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Result
No.
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have score of the result being printed, and is derived by analysis of the total score distribution.
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                          Match
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US-09-086-118-23
US-09-835-684-3
US-09-880-371-3
US-09-879-248-3
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5393.494 Million cell updates/sec
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Sequence 23,
Sequence 3, A
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                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                ZIP: 14603
                                                                                                                                                                                                                              STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                          STATE: New York
    CLASSIFICATION
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Sequence II, AppI	S-09-770-695-				165
Seguence 40290, A	US-09-864-761-40290	16 10	116	6.4	166
Sequence 36985, A	S-09-864-761-				56.5
Sequence 24, Appl	78-547-24				168
Sequence 13, Appl	S-09-770-693-1				169
Sequence 215, App	-10-108-605-				171
Sequence 2, Appl1	10-078-547-				2.5
Sequence 1068, Ap	S-09-833-263-106	79 10			4.5
Sequence 1068, Ap	-09-922-217				4.5
Sequence 1068, Ap	10-025-380-3				
Sequence 202, App					4.5
Sequence 52, Appl		10 12			.5
Sequence 52, Appl					. 5
Sequence 106, App					4.5
Sequence 8, Appli	۵				176
Sequence 2, Appli					6.5
	US-09-925-299-1002			7.1	183
				7.6	2.5
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Sequence 35807, A	US-09-864-761-35807	57 10		7.8	7.5
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equence	US-09-879-248-15	10			7.5
	US-09-880-371-11	10			7.5
1, App	US-09-835-684-11	10		7.8	7.5
27	US-09-086-118-27	5			7.5
Ļ	US-09-835-232-1	10			202
8, Appl	US-09-861-597-8	10			5
6,	US-09-861-597-6	5		8	5
e 2, Appl	US-09-835-232-2	5			212
e 1, Appl	US-09-861-597-1	5			ω .5
	US-10-086-464-17	9		8.5	220
2, Appl	US-09-823-240-2	10			4.5
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: 1, Appl	-09-87		ω		8
۲	-09-88		ω u	28.4	
٢	S-09-835-684-	10	ω	28.4	8.5
21	-09-08		33	28.4	8
Sequence 3, Appl1	S-09-766-348-	ω	40	82.1	079
G	S-09-770-693-	w	40	B2.1	079

ALIGNMENTS

Sequence 21, Application US/0006118
Fatent No. 18230101180A1
RECENT NO. 18230101180A1
RECENT NO. 18230101180A1
APPLICAMI: New York Stewent V.
APPLICAMI: New York Stewent V.
TITLE OF INVENTION: PRESENSITIVE RESONER ELICITION
TITLE OF INVENTION: PRESENSITIVE RESONER ELICITION
TITLE OF INVENTION: PRESENSITIVE RESONER AND USES
LITTLE OF INVENTION: PRESENSITION: PRESENSITIVE RESPONSE AND USES
LITTLE OF INVENTION: PRESENT NEW YORK OF THE PRESENSITIVE RESPONSE AND USES
LITTLE OF INVENTION: PRESENT

MBER OF SEQUENCES: 30

BRESSORNENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CTTV. Brobester

SANE: Mewhere
SANE: Mewhere
COMPRET: U.S.A.
COMPRET: U.S.A.
COMPRETE: U.S.A.
COMPRETE: C.S.A.
MEDIZING PITCH: POPPY disk
MEDIZING PITCH: POPPY disk
MEDIZING PITCH: POPPY disk
MEDIZING PITCH: MEWHERE
STREMMER: MEMORIAN BOOKS
SOFTWARE: MEMORIAN BOOKS
SOFTWARE: MEMORIAN BOOKS
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SEQ12-SEQ4 (1-1390) x US-09-086-118-23 (1-403)
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TELEPHONE: (716) 263-1304
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 6
PILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
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                                                                    181
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1 MetserLeunsnfhrserGlyLeuGlyAlaSerThrWetGlnTleSerIleGlyGlyAla 20
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STRANDEDNESS:
TOPOLOGY: 11
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REGISTRATION NUMBER: 30,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 403 amino acids
GlyValThrAspAlaLeuSerGlyLeuMetGlyAsnGlyLeuSerGlnLeuLeuGlyAsn
                             GGAGTCACTGATGCGCTGTCGGGCCTGATGGGTAATGGTCTGAGCCAGCTCCTTGGCAAC 834
                                                                                 CAGGGCAGTTCCTCTGGGGGCAAGCAGCCGACCGAAGGCGAGCAGAACGCCTATAAAAAA 774
                                                                                                                                                                                                                                                                                                                            GGGGGGGGCTTNGGTANTGGCTTGGGTGGCTCNGGTGGCCTGGGCGANGGACTGTCGANC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnGlySerSerGlyGlyLysGlnProThrGluGlyGluGlnAsnAlaTyrLysLys
                                                                                                                           CTGCTGANGATGTTCAGCGAGATAATGCAAAGCCTGTTTGGTGATGGGCAAGATGGCACC 714
                                                                                                                                                                                                AACGACGATTCCACCTCCGGCACAGATTCCACCTCAGACTCCAGCGACCCGATGCAGCAG
                                                                                                                                                                                                                                                                 ThritheserThritheserFroieuAspGlnAlaLeuGlyIleAsnserThriserGln 140
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Matches:
Conservative:
Mismatches:
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SEQ12-SEQ4 (1-1390) x US-09-835-684-3 (1-403)

Gaps:

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Best Local Similarity:
Query Match:
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                                                                                                  Pred. No.:
                                                                                                                 Alignment Scores:
                                                                                                                                                       US-09-835-684-3
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                                                                                                                                                                                                                                  SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. US20020019337A1
                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/835,684
CURRENT FILING DATE: 2001-04-15
PRIOR APPLICATION NUMBER: 66/198,359
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PREVENTIN FET. 2.1
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Remick, Dean
TITLE OF INVENTION: TREATMENT OF PRITTS OR VOSETABLES WITH HYDESGROWSTATE
TITLE OF INVENTION: RESPONSE BLICITOR TO CONTROL POSTMANVEST DISEASE OR
TITLE OF INVENTION: DESICOTION
TLLE REFERENCE: 2,1829/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wei, Zhong-Min
APPLICANT: Qiu, Dewen
                                                                                                                                                                      ORGANISM: Erwinia amylovora
                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1075 GGTCAGTTCATGGACCAGTATCCTGAGGTGTTTGGCAAGCCGCAGTACCAGAAAGGCCCG 1134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProMetAlaGlyAspThrGlyAsnGlyAsnLeuGlnAlaArgGlyAlaGlyGlySerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyAlaAla 403
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360	1 AspClyMetThrProAlaSerMetGluGlnPheAsnLysAlaLysGlyMetIleLysArg	(43	망
1254	GACGGAATGACACCAGCCAGTATGGAGCAGTTCAACAAAGCCAAGGGCATGATCAA	1195	é
340	GlyGlnGluValLysThrAspAspLysSerTrpAlaLysAlaLeuSerLysProAspAsp	321	몽
1194	GGTCAGGAGGTGAAAACCGATGACAAATCATGGGGCAAAAGCACTGAGCAAGCCAGATG	1139	Qy
320	GlyGlnPheMetaspGlnTyrProGluValPheGlyLysProGlnTyrGlnLysGLyPro	301	Ъ
1134	GTCAGTTCATGGACCAGTATCCTGAGGTGTTTGGCAAGCCGCAGTACCAGAAAGGCC	1075	Qy
300	ArgHisSerSerThrArgSerPheValAsnLysGlyAspArgAlaMetAlaLysGluIl	281	Ф
1074	AGGCACAGTTCAACCCCTTCTTTCGTCAATAAAGGCGATCGGGCGATGGC	1019	Qy
280	ValGlyThrGlyIleGlyMetLysAlaGlyIleGlnAlaLeuAsnAspIleGlyThr	261	Db
1014	GTGGGTACCGGTATCGGTATGAAAGCGGGCATTCAGGCGCTGAATGATATCG		ş
260	GlyGlyLysGlyLeuGlnAsnLeuSerGlyProValAspTyrGlnGlnLeuGlyAsnAla	241	Db
954	CANAGGGCTGCAAAACCTGAGCGGGGCGGTGGACTACCAGCAGTTAGGTAACGCC	895	9
240	lyThrGlyLeuAspGlySerSerLeu	221	Db
894	SACTOGGAGGTGGTCAGGGCGGTAATGCTGGCACGGGTCTTGACGGTTCGTCGCTG	835	9
220	lyAsnGlyLeuSerGlnLeuLeuGlyAsn	201	B
834	AGTCACTGATGCGCTGTCGGGCCTGATGGGTAATGGTCTGAGCCAGCTCCTTGGCAAC	775	Q
200	GlnGlySerSerGlyGlyLysGlnProThrGluGlyGluGlnAsnAlsTyrLysLys	181	Db
774	AGGGCAGTTCCTCTGGGGGCAAGCAGCGGGGGGGGAGCAGAACGCCTATAAAAAA	715	9
180	LeuLeuLysMetPheSerGluIleMetGlnSerLeuPheGlyAspGlyGlnAspGlyThr	161	₽
714	AAGATGTTCAGCGAGATAATGCAAAGCCTGTTTGGTGATGGGCAAGATGGCACC	655	9
160	AsnaspaspSerThrSerGlyThrAspSerThrSerAspSerSerAspProMetGlnGln	4	Db
654	ACGACGATTCCACCTCCGGCACAGATTCCACCTCAGACTCCAGCGACCCGATGCAGCAG	595	ş
140	rSerGln	121	용
594	CCACTTCAACAACAAATTCCCCCGCTGGACCAGGCGCTGGGTATTAACTCAACGTCCCAA	535	8
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534	CGCTGAACGATATGTTAGGCGGTTCGCTGAACACGCTGGGCTCGAAAGGCGGCAACAAT	475	Qγ
100	GlyGlyGlyLeuGlyAsnGlyLeuGlyGlySerGlyGlyLeuGlyGluGlyLeuSerAsn	82	В
474	GCGGTGGCTTAGGTAATGGCTTGGGTGGCCTCAGGTGGCCTGGGCGAAGGACTGTCGAAC	415	g.
80	lyGlyGlyLeu	61	용
414	CCGCCATGATGATGATGATGACCATGATGGCCGGTGGTGGCTGATGGCCGGTGGCTTA	355	Ωy
60	AlaLeuGlyLeuGlyGlyAsnGlnAsnAspThrValAsnGlnLeuAlaGlyLeuLeu	41	₽
354	GGGGCTGGGCGGGTAATCAAAATGATACCGTCAATCAGCTGGCTG	ū	ş
40	GlyGlyAsnAsnGlyLeuLeuGlyThrSerArgGlnAsnAlaGlyLeuGlyGlyAsnSer .	ï	Db
294	NAATAACGOGTTGCTGGGTACCAGTCGCCAGAATGCTGGGTTGGGT	C)	δ
	MetSerLeuAsnThrSerGlyLeuGlyAlaSerThrMetGlnIleSerIleGlyGlyAla		₽ 5
234	ACTOTAATACAAGTGGGCTGGGAGCGTCAACGATGCAAATTTCTATCGGCGGTGCG	175	Ş

CAGCAG 654	5 AACGACGATTCCACCTCCGGCACAGATTCCACCTCAGACTCCAGCGACCCGATGC	59	9
SerGin 140	1 ThrThrSefThrThrAsnSerProLeuAspGlnAlaLeuGlyIleAsnSerThrSerGln	12	D.
TCCCAA 594	5 ACCACTTCAACAACAAATTCCCCGGCTGGACCAGGCGCTGGGTATTAACTCAACG	53	9
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AACAAT 534	5 GCGCTGAACGATATGTTAGGCGGTTCGCTGAACACGCTGGGCTGGAAAGGCGGC	y 47	Q
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Y-199	NS/	COMPUTER: ELOPPY GISK COMPUTER: IBM PC COMPACT OPERATING SYSTEM: PC-DOS SOFTWARE: Patentin Relea	*	E: Nixon, Hargrave, Clinton Square, P.O. ochester	THEREOF	Laby, Ronald J. Beer, Steven V. Wei, Zhong-Min	us/0		WIGATG	hrely	Maser	GCAGE	ACCGAT	CAGTAT	rgSer	GTTCT	SGTATO	SinAsc	CA.A.A.A.C	SGTCAG	LeuSea
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Length: 338 Matches: 173 Conservative: 41 Mismatches: 111 Indelshes: 79 Gaps: 11	98: 1.29e-45 718.50 City: 52.97% Llarity: 42.82% 10.38%	Alignment Score Pred. No.: Score: Percent Simila: Best Local Sim: Ouery Match: DB: CRO12-SR04 (1	«eroermon
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9	SEQ12	Alignme Pred. N Score: Percent Best Lc Query M DB:	PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	Db 09	B Q	Db Oy	Db Oy	Oy Db	B 8	Db 04	D Q
211	2-SEQ4	Me Local	1372 CT 009-835-61 009-835-61 009-835-61 009-835-61 009-835-61 009-835-61 1335 LII 1335	1312	1252 295	1192 275	1132 255	1072 235	1012 215	195	892 175
ATGCAAATTTCTATCGGCGGTGCGG	04 (1-1390) x US-09-835-684-1 (1	Scores: 1.29e-45 : 718.50 Indianity: 52.97% I Similarity: 42.82% ch: 28.38%		TGGCTGGGTATTGATGCCATGATGGCCGGTGATGCCA	aggcccaTggcgggTsATaccggCaAcggc ::: SeralaValAlaGlyAspThrGlyAsnThr	GACGACGGAATGACACCAGCCAGT	CCGGGTCAGGAGGTGAAAACCGATGACAAA 	: ATCGGTCAGTTCATGGACCAGTATCCTGAGGTG:	CACAGGCACAGTTCAACCCGTTCTTTCGTCAA	GCCGTGGGTACCGGTATGGGTATGAAAGCGGGCATTC	Ciogocogcanagescigcananccreaccogcaccogregactaccascactiness
AACGGGTTGCT	-338)	Length: 338 Matches: 173 Conservative: 41 Mismatches: 111 Indels: 79 Gaps: 11	S ON VERTALLES. TO CONTROL POS	ATTAACAATATO	E = 3	ATGGAGCAGTTCAACAAAGCCAAGGGC ::::: ::: MetasplysPheargGinalametGly	TCATGGGCAAAAGCACTGAGCAAGCC 	PTTGGCAAGCCGCAGT	TARAGGCGATCGGGCC : pLysGluAspArgGl;	AGGCGCTGAA1	GGGCCGGTGGACTACCAGC
SGGTACCAGTCGC 267			HAVEST DISEASE OF	GCACTTGGCAAG 1371 ::: SerLeuGlyLys 334	CCGGTGGTTCT 1311	GCATGATCAAA 1251 	GCAAGCCAGAT 1191 erLysProAsp 274	ACCAGAAAGGC 1131 yrGlnLysAsp 254	ATGGGGAAGGAA 1071 MetalaLysGlu 234	rgATATCGGTACG 1011 :::::::: :AsnValSerThr 214	AGTTAGGTAAC 951 nLeuGlyasn 194

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RESC US-1 PR	B 8	DP OA	B 03	B 8	D 99	P 0y	Db Qy	D 9	B 9	Db Qy	Db Oy	Db Oy	ОУ
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113	234	107	101	194	174	167	831	8	128	711	108	675	æ	615	6	555	82 495	ω	435	C)	75	8	5	0	67				

APPLICANT: Wel, Zhong-Min APPLICANT: Wel, Zhong-Min		Qy 436 TTGGGTGGCTCAGGTGGCCTGGGCGAAGGACTGTCGAACGCGCTGAACGATATGTTAGGC 495
MSSULT 12 US-09-766-348-1 : Sequence 1. Application US/09766348	· · · · · · · · · · · · · · · · · · ·	QY 376 AGCATGATGAGCTGATGAGCCGTGGCTTAGGCAGTGCCTTAGGTAATGAC 435 Db 56
11/2 CTGGGCGGGGT 1183	B 9	Qy 316 AATCAAAANGATRACGGTCAATCAGGTGGCTTACTCACCGGCATGATGATGATGATGATGATGATGATGATGATGATGATGA
111 TOCOTOGOTATTOATCCATGANGGCOGGGAAGCAATMGCCATGCGAAG 171 111 TOCOTOGOTATTOATCCATGANGGCCGGGAAGCAATMGCCATGCGAAGGAATAGCAATMGCCATGAAGAATMGCCATGAAGAATMGCAATGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	315 Qy 38 pb	Qy 268 CAGAMICTGGGTTGGGTGGCAMTITTGGATGGGGGTGGGGGGGGG Db 21 GlnClysablyGGlyLaukhGelAlalaSerSerLauGlyerSgrvalasp
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952 GCCGTGGGTACCGGTMYCGGTMYCGAAACCGGGCATAAACCGGCACAAACGAAACAGGCAAAACCGGCACAAACGAAACCGGCACAAACCGGCACAAACCGGCAAAACCGGCAAAACCGGCAAAACCGGCAAAACCGGCAAAAACCGGCAAAAACCGGCAAAAAA	Db Db	WIGH APPLICATION WHERE: 6/0/178.565 PRIOR APPLICATION WHERE: 6/0/178.565 PRIOR APPLICATION WHERE: 6/0/1-26 PRIMER PILING DATE: 2000-01-26 PRIMER PILING DATE: 2000-01-26 PRIMER PILING DATE: 2000-01-26
892 CTGGGCGGCAAAGGCTGCAAAACCTGAACGGGCGCGGTGGATAACCAGCAGCTAAGTAAC 951	Db Db	TITLE OF INVENTION. PRIMOGENTATION DE EXPRESSION OF A METENDIAGOUS FITLE OF INVENTION. PRIMOGENTATIVE RESPONSE ELICITOR FITLE REFERENCE: 19603/2501 ENTENTIVE RESPONSE ELICITOR CURRENT APPLICATION MUMBER: US/09/770,693
832 ANGGGGGANTTGGGAGGTGGTCAGGGGGTTATTGCTGGCACGGGTTCATCG 891 168	Db Db	**************************************
772 ANAGARTRACTARGOCCISTOGGCCISAYGGCTAMTGGTCTRAGCCACCTCCTTCGC 831	Db Db	US-09-770-693-1 US-09-770-693-1 Sequence 1. Application US/09770693 Sequence 1. US/00200543441
712 ACCCAGGCAATTCCTCTGGGGGCAAACACACACACACACA	Qy	CY 12 CTWOCCCCCCCT 1383 Db 335 LeuAlahsnAla 338
676 ATANTOCAMAGCCTTTTGGT	NAG 1371 QY	315
616 ACAGATTCCACCTOCAGCTCCAGCGACCAGCTGCTGCAGAGATGTTCAGCGAG 675	TCT 1311 Qy	295
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496 GGTTGGGTGAACAGGTGGAAAGGGGGGAAAGGGGGGAAAGGAGTGAACAAGAAAATTGC 555 83 ASNGlyAlaGlnGlyAlaSerAenLeuLeuSerVslproLye 96	GAT 1191 Qy 	Qy 1132 CCGGGTCARGAAGTGAAAACCGATGACAAATCAATCGCAAAACCACTGACCAAACCACTGACCAAACCAAATCAAATCAAATCAAATCAAAACCACTGACCAACCA
64 LeuGlyAlaSerSerLysGlyLeuGlyMetSerAsnGlnLeuGlyGlnSerPheGly 82	Asp 254 Db	-
Page J	seq12-seq4.n2p.rapb	Wed Jan 15 11:31:39 2003

167 B91	2 9	Db 14 Qy 83	
831	72 AAAGGAGTCACTGATGCCCTTCCGGCCCTGATGGGTAATGGTCTGAGCCACCTCCTTGGC	Qy 7	
771 148	12 ACCCAGGGCAGTTCCTCTGGGGGCAAGCAGCGCGAAGGCGAAGAAGACGCTATAAA .29 LGUALAAASNSETMETLGUÄSNÄLASETGINMETTATGINGIYÄSNMETASNÄLAPNEGIY	Oy 71	- 0
711	6 ATAATGCAAAGCTCTTTGGT	Oy 676 Db 109	- 0
108	6 ACAGATYCCACCYCAGACYCCAGGGACCGGATGCAGCAGCYGGTGAAGATGTTCAGCGAG ::: ::: ::: 9 Glyaspalaleuser	Oy 616	- 0
98	6 CCGCTGGACCAGGCGCTGGGTATTAACTCAACGTCCCAAAAGGACGATTCCACCTCCGGC	Qy 556 Db 97	
96	6 GGTTCGCTGAACACGCTGGCTCGAAAGCGCAACGACTGAATACCACTTCAACAACAAAAATTCC 3 ASNGlyAlaGlnGlyAlaSerAsnLeuLeuSerValProLys	Qy 496 Db 83	п О
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	Allamant Scores: 1.28e 45 Length: 338 Pred. Mo.: 1239 MacChest 1.28e 1.29 Score: Establity: 42.23 MacChest 1.2 Best Local Smilarity: 42.23 Massaches: 11 Best Local Smilarity: 42.23 Massaches: 11 Georgy Match: 23.38 Indels: 75 Best Local Smilarity: 42.23 Massaches: 11 Georgy Match: 10 Gapts: 11	Alignment Pred. No Score: Percent : Dest Loca Query Mai	9099999
PLANTS BY	Bear, Steven V. WORSTON - HYPERSHSITTIVE RESPONSE INDUCED RESISTANCE IN WORSTON - SOURCE FROM A STATE FRICATION NUMBER 10, 90,0746,148 LICAR DATE: 2001-01-19 LICAR DATE: 1996-1-05 LICAR DAT	APPLICAM: TITLE OF I TI TITLE OF I TITLE OF	5

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802 113 32 31 1166 1166 20	ting Cell		TATGGCACTTGGCAAG ::: nMetSerLeuGlyLys	GGTGCCGGTGGTTCT GlyAlaGlyGlyAla	AAGGGCATGATCAAA MetGlyMetIleLys	CTGAGCAAGCCAGAT	CAGTACCAGAAAGGC ::: GluTyrGlnLysAsp	GCGATGGCGAAGGAA GlyMetAlaLysGlu	AATGATATCGGTACG	CAGCAGTTAGGTAAC 	::: -SerGlyPheSerGlnProSer
			1371	1311	1251 294	1191 274	1131 . 254	1071	1011	194	174

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Alignment Scores:	US-09-861-597-1		SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1	PRIOR FILING DATE: 1998-02-11 NUMBER OF SEQ ID NOS: 14	PRIOR FILING DATE: 1999-02-11 PRIOR APPLICATION NUMBER: FR 98/01614	-22 247, 806	FILE REFERENCE: 6388-0365-0 CURRENT APPLICATION NUMBER: US/09/861,597	TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN TITLE OF INVENTION: ANALOG	2	APPLICANT: PHILLIPPE, Michel	Patent No. US20020064539A1 GENERAL INFORMATION:	- Seriesce 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	2 870 dt 270	3 1	223 TA 222		277 CAGCATTCTGGCGACTGGTACCCAGCAACCCGTTATTTCCGCCCGCACCCGCA		337 CARTROLOGORAGO MATERIAL DO COLO COLO COLO COLO COLO COLO COLO		207 (777) (77		439 CCAMC		499 AACCGCCTAACATATCGTTCAGCGCCCTTTCGACAGTGCCTTTCGCCCAAGCCCAACCCAC	167 1vProtys	SEQ. COCCOLATOR PROPERTY CONTRACTOR CONTRACT	147 print Proproval Assithatia Serperopropropropropropropropropropropropropr	619 CTGTGCCGGAGGTGGAATCGTCGTTTTGGGAACGTTAATTAA	142	679	124 erProProSerGluThrValProProGlyAsnThrIleSerProProProArg 141	739 GCTTGCCCCCAGAGGAZ		799 GGCCCGACAGCGCATCACTGACTTCTTTTTTTTATAGGCCTTTCTTCTCCTTTC	90 roProLeuGluSerProSerProProSerProHis
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359 GLn		339 GlyAl	982 GGCAT	322 GlyGl	922 GGGCC	302 GlySe	874 GGTCT	284	823 CTCCT	270	763 GCCTA	257 GlyLe	703 CAAGA	254	643 CCGAT	235 GlyAL	583 TCAAC	215 AlaG1	526 GGCAA	203	466 CTGTC	184 TyrGl	412 TTAGG	164 LeuG1	352 CTCAC	144 GlyGl:	301 GG	124 G1yG1	253 CTGGG	104 GlyGl	193 GGGCT	SEQ12-SEQ4 (1-1		Best Local Simi Query Match:	Score:	Pred. No.:

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or lumarium darkari memarianianiani	359 Gin	1041 CARTAAAGGCGATCGGGCGATGGCGAAGGAAATCGGTCAGTTCATGGAC	339 GiyalaalaalaalaalaGiyGlyAlaGiyGinGiyGiyTyrGiyGiyLeuGiySer 358	982 GGCATTCAGGCGCTGAATGATATCGGTAC-GCACAGGCACAGTT	322	922 GGGCCGGTGGACTACCAGCAGTTAGGTAACGCCGGTGGGTACCGGTATCGG	302	874 GGTCTTGACGGTTCGCTCGCTGGGCGGCAAAGGGCTGCAAAACCTGAC	284GlyTyrGlyGlyLeuGlyGlyGln	823 CTCCTTGGCAACGGGGACTGGGAGGT	270AlaGlyAlaAlaAlaAlaAlaA	763 GCCTATAAAAAAGGAGTCACTGATGCGCTGTCGGGCCTGATGGGT	257 G	703 CANGATGGCACCCAGGGCAGTTCCTCTGGGGGCAAGCAGCC	254 GlyTy	643 CCGATGCAGCAGCTGCTGAAGATGTTCAGCGAGATAATGCAAAGCCTGTTTGGTGATG	235 GlyAlac	583 TCAACGTCCCAAAACGACGATTCCACCTCCGGCACAGATTCC	215 AlaGlyAlaAla	526 GGCAACAATACCACTTCAACAACAAATTCCCCCGCTGGACCAG	203GlnGlyAlaGlyArgGlyGlyLeuGlyGl	466 CTGTCGAACGCGCTGAACGATATGTTAGGCGGTTCGCTGAACACGCTGGGCTCGAAAG	184 TyrGlyGlyLeuGlyGlyGlnGly	412 TTAGGCGGTGGCTTAGGTAATGGCTTGGGTGGCTCA		352 CTCACCGGCATGATGATGATGAGGATGATGGGCGGTGGTGGGCTGATGGC	Db 144 GlyGlyAlaGlyGlyGlyTyrGlyGlyLeuGlySerGlnGlyAlaGlyArgGlyGly 163	301 -	Db 124 GlyGlyLeuGlyAsnGlnGlyAlaGlyArgGlyGlyGlnGlyAlaAlaAlaAlaAlaAla 143	253 CTGGGTACCAGTCGCCAGAATGCTGGGTTGGGTTGG	Dy 193 GGC/GCGGGCCTCAACGATGCAATTC:NTCGGCCGGTGCGGGCGGAATTACGGTTG 252	EQ12-SEQ4	Pred. No.: 2.11c-38 Langth: 651 Roce: 1.00 million 1.00 million 1.00 million Roce: 1.00 million 1.00 million 1.00 million

- S, B 망 Š Db 20 рb Search completed: January 14, 2003, 17:18:53 Job time : 18 secs 1161 ATCATRGGCALANACCACTRACCAGCANTGACCAGGCANTGACACCAGCCAGTNTGGA 1220
 389 -----GlyLeuGlySerGlnGlyAla-----GlyArgGlyGlyGlyGlnGlyAlaGlyAla 404 1338 CGGTGATGCCATTAACAATATGGCACTTGGCAAGCTGGGC 1377 1381 CARCTTGCAGGCACGTGCC --GGTGGTTCTTCGCTGGGTTATTGATGCCTATGATGGC 1337 1221 GENGTTCANCAMGCANGGGCATGATCANAGGGCTGATGGGGGTGATACCGGGAACGG 1280
 405 AlaalaalaalaalaGlyGlyAlaGlyGlnAtgGlyTyTGlyGly-----LeuGlyAsn 422 442 aAlaGlyGlyAlaGlyGlnGlyGlyTyrGlyGlyLeuGly 455

2079 82.1 400 2 US-08-200-724.2 2079 82.1 400 2 US-08-200-724.2 2079 82.1 400 2 US-08-200-270.3 2079 82.1 400 4 US-08-200-270.3 2079 82.1 400 4 US-08-200-270.3 2079 82.1 400 4 US-08-200-270.3 2079 82.1 400 4 US-08-200-270.3 208-2 US-08-200-270.3 208-2 US-08-200-270.3 208-2 US-08-200-270.3 208-2 US-08-200-270.3 208-2 US-08-200-270.3 208-2 US-08-200-270.3 208-2 US-08-200-270.3 208-2 US-08-200-270.3	score greater than or equal to the force of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES DEFINE DOES DOES	Disable: Issued_Petents_AN. Yes_Petents_AN. Yes_Petents	CAVER 1_UNERTO SPOOK_PREENTS()/LOUDE_LOUDE_LOUDE_LOUDE_SCHEET_) OPH_SEMON_PREENTS_CALL_OPENT_CALL_	Post-processing Hiniman Macch 08. Post-processing Hiniman Macch 1001 Maximum Macch 1001 Maximum Maximum Macch 1001	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Total number of hits satisfying chosen parameters: 525148	Searched: 262574 seqs, 29422922 residues	Scoring table: BLOSH020 , Napper 0.5 spaper 10.0 , Napper 0.5 spaper 0.0 , Napper 0.5 spaper 0.0 , Napper 0.0 pelpop 6.0 , Napper 7.0	Title: SB012-SB04 Perfect score: Z532 Sequence: 1 atgggattttttctctttttcgctgggcgcggcttaagctt 1390	Run on: January 14, 2003, 17:09:17, search time 13.5 seconds (vithout alignments) 6058-942 Million cell updates/sec	OM nucleic · protein search, using frame_plus_n2p model	GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compayen Ltd.	Wed Jan 15 11:31:38 2003 seq12-se
COMPUTER: IBM PC COMPANIAN OPENTATION SYSTEM E-COMPANIAN OPENTATION SYSTEM E-COMPANIAN COMPUTER: COMPANIAN APPLICATION NUMBER: 105/08/200,724A PILING NATE: 33 PSB-198/4/200,724A PLING NATE: 33 PSB-198/4/200,724A CLASSIFICATION SIGNED PROPRESSION SIGNED PROP	STREET: Clinton Square CITY Rochester STATE: New York STATE: New York COMPTER REALMER FOOK: MEDIUM TYPE: IDDRY dik MEDIUM TYPE: IDDRY dik	Beer, St. Collmer, He, Shen Laby, Ro VENTION: VENTION: EQUENCES: EQUENCES:	ALIGNMENTS BESUT 1 774A-2 US-08-200-724A-2 US-08-200-724A-2 US-08-200-724A-2 US-08-200-724A-2 Patch Ev. S-54-2688 Patch Ev. S-54-2688 APPLICATE: Baser David M. APPLICATE: Baser David M.	4) 197.5 7.8 344 1 US-08-891-254-7 42 197.5 7.8 344 2 US-08-1891-393-7 43 197.5 7.8 344 2 US-09-010-270A-7 44 197.5 7.8 344 4 US-09-010-270A-7 45 197.5 7.8 344 4 US-09-013-587-7	200.5 7.7 174 4 US-08-818-111-138 Sequence 200.5 7.7 174 4 US-09-056-556-143 Sequence 200.5 7.7 174 4 US-09-072-556-138 Sequence	36 201 7.8 1315 3 US-08-899-595-3 Sequence 37 200.5 7.7 174 4 US-08-818-112-143 Sequence	34 201 7.8 1248 2 US-09-080-897-2 Sequence 35 201 7.8 1248 4 US-09-323-735-2 Sequence	8.1 606 4 US-09-247-806-8 Sequence 7-9 1255 2 US-09-0800-897-4 Sequence 7-9 1255 3 US-09-899-555-1 Sequence 7-9 1255 4 US-09-237-735-4 Sequence 7-9 1254 4 US-09-060-756-728 Sequence 8-0 344 4 US-09-060-756-728 Sequence	211. 8. 4. 318. 4. US-09-061-756-727 211. 8. 738. 3. US-08-964-738-3. Sequence 211. 8. 738. 3. US-08-247-806-6. Sequence 204. 5. 8. 1. 606. 4. US-09-247-806-5. Sequence 204. 5. 8. 1. 606. 4. US-09-247-806-6.	213.5 8.4 651 4 US-09-247-806-1 Sequence 213.5 8.4 718 1 US-08-317-9649-2 Sequence 213.5 8.4 718 2 US-08-317-9448-2 Sequence 213.5 8.4 747 3 US-09-034-177-3 Sequence	718.5 28.4 548 5 PCT-US56-08813-1 Segmence 213.5 8.4 604 4 US-08-556-9788-63 Segmence 213.5 8.4 651 4 US-08-556-9788-19 Sequence	338 2 US-09-030-270A-1 338 3 US-09-011E-959-2 338 4 US-08-984-207-1 338 4 US-08-013-587-1	seq12-seq4.n2p.xai Page 1

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SEQ12-SEQ4 (1-1390) x US-08-200-724A-2 (1-403)
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MOLECULE TYPE: peptide
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LENGTH: 403 amino acid
                              895 GGCGCAMAGGCTGCAMACCTTCAGCGGCCGGTGGKCTNCCAGCAGTAGTTAGCGC 954
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                                                                                                             GGGGGACTGGGAGGTGATCAGGGCGGTAATGCTGGCACGGGTCTTGACGGTTCGTCGCTG 894
                                                                                                                                                                                    GlyValThrAspalaLeuSerGlyLeuMetGlyAsnGlyLeuSerGlnLeuLeuGlyAsn 220
                                                                                                                                                                                                       GGAGTCACTGATGCGCTGTCGGGCCTGATGGGTAATGGTCTGAGCCAGCTCCTTGGCAAC B34
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: Patent No. 5977060
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                                                                                                   TELEFAX: (716) 263-16
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 60,
FILING DATE: 28 -FEB-1997
APPORNEY/AGENT INFORMATION:
ANNEWS/AGENTAGENSAGEN
                                                                                                                                                             REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zitter, Thomas A.
APPLICANT: Wei, Zhong-Min
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                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: INSECT CONTROL WITH A TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
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STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
TOPOLOGY: 1:
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281 ArgHisSerSerThrArgSerPheValAsnLysGlyAspArgAlaMetAlaLysGluIle 300

OBESTICA 3 LANGUAGE CONTROLLED CO	1375 GGCGGGGCT 1383 401 GlyAlaAla 403	1315 CTGGGTATTGATGCCASTGATGGCCGSTGATGCASTTACAAAGTGGCACTTGGAAGCTGT 1361 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1255 CCANGGCGGGTGANMCCGCAACGGCAACCTGCAGCGACGGGTGCCGGGTGCTGCTGCG 1255 CCANGGCGGGTGANMCCGCAACGGCAACGGCGGTGCCGGGTGCTGCTGCGG 1257 CCANGGCGGTGANGGCGAACGGCAACGGCGAACGGCGGTGCGGGTGCGGGTGCGGGTGCGGGTGCGGGTGCGGGTGCGGGTGCGGGTGCGGGTGATGATGGTGAACGGAACGAAC	1195 GACGGARTGAACCAGCAGTATGAACAAGTCAAGGGCATGATCAAACAGGCATGATCAAAAGCCAAGGCCATGATCAAAAGCCAAGGCCATGATCAAAAGCCAAGGCCATGATCAAAAGCCAAGGCCAAGGCCAAGGCCAAGACCAAGGCCAAGACCAAGGCCAAGACCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGACCAAGGCCAAGAGCCAAGAGCCAAGAGCCAAGAGCCAAGAGCCAAGAGCCAAGACAAGCCAAGAGCCAAGACAAGCCAAGACAAGCCAAGACAAGCCAAGACAAGCCAAGACAAGCCAAGACAAGCCAAGACAAGCCAAGACAAGCCAAGACAAGCCAAGACAAGCCAAGAAG	1135 GGTCAGGAGGTGAAACCGATGACAATCATGGGCAAAGCACTGAGCAGAGCGAGATGAC 	1075 GGTCAGTTCATGGACCAGTATCCTGAGGTGTTTGGCAAGCCGCAGTACCAGAAGGGCCGG
TE RESPONSE		GGCACTTGGCAAGCTG 1374 tAlaLeuGlyLySLeu 400	TGCCGGTGGTTCTTCG 1314 	GGGCATGATCAAAAGG 1254 	GAGCAAGCCAGATGAC 1194 	GTACCAGAAAGGCCCG 1134

1134	GTCAGTCATGGACCAGTATCCTGAGGTGTTTGGCAAAGCGGAATACGAGAAAGGCCG 	Qy 1075 Db 301	
300	ACHIEF THE ACCOUNT OF THE ACTION OF THE ACTI	Db 281	
280	TUGSTACUSTRICUSTRIGAAAGUGGCRITCAGGCCTGAATGARARACGGRACGC TUGSTACUSTRICUSTRIGAAAGUGGCRITCAGGCCTGAATGARACGCRACGGRACGCRACGGRACGGR	26 3	
260	LULUKAMAGASCINCAMAKCINAKCUGGICUGTGACTACOKOKATTAGGTAGGT 	2 0	
240	ARCTOGRAGGTEGTEAGGGCGGTMATGCTGGCACGGGTCTGAGGGTTCGTCGCTG 	2 83	
834	GGAGTCACTONTGCGCTGTCGGGCCTGATGGGTAATGGTCTGACCCAGCTCCTTGGCAAC	Oy 775 Db 201	
774	CAGGGCAGTTCCTCTGGGGGCAAGCAGCCGAAGGCGAAGAGAAGACGCCTATAAAAA 	Oy 715	
714	CTCCTSANGATGTTCAGCGACATMATGCAAACCTTTTGGTGATGGGGAAACTGGGGACTGGGGCAACATGGGGCAACATGGGGCAACATGGGGCAACATGGGGCAACATGGGGCAACATGGGGCAACATGGGGCAACATGGGGCAACATGGGGCAACATGGGGCAACATGGGGCAACATGGGGATGAAGAGGAAACATGAAAAAAAA	Qy 655 Db 161	
160	ARGACGATTCCACCTCCGCALAAATTCCACCTCAAGCTCCACGACCGATGACCCATGACCTCAAGACTCCACCTCAACTCCACCCAC	Oy 595	
594 140	ACCACTCAACAACAATTCCCCCCTGGACCAAGGCCTGGGTATTAACTCCAAGGTCCGAAGGACGTGGGTATTAACTCCAAGGTCCGACAAGGACGTTGGTATTAACTCCAAGGTCCGACAAGGTCCTGAACTAACT	Оу 535 Db 121	
534 120	GCCTTAACGATATGTTAGGCGCTTACGCCTCGACACCCTCGGCTCGAAAGGCGCCAAAGGCTCGAAAGGCGCAAAGGCGCAAAGGCGCAAAGGCGCAAAGGCGCAAAGGCGCAAAGGCGCAAAGGCAAAGGCAAGGCAAAGGCAAGAGGCAAAGGCAAGAGGAAAGGCAAAGGCAAGAGAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAA	Oy 475	
100	GLYGLYGLYLEUGLYASAGTATGCCTTGCCCTAGGCAAGGACGCTGCCCAAGGACGCTGCCCAAGGACGCTGCCCCAAGGACGCTGCCCCAAGGACGCTGCCCCAAGGACGCTGCCCCAAGGACGACGACGACGACGACGACGACGACGACGA	Oy 415 Db 81	
414 80	ACCGGCATGATGATGATGAGCATGATGGGCGGTGGCTGATGGCGGTGGCTTA	Oy 355	
354	GCACTGGGGCTGGGCGGGGTAATCAAAATGATACGGTCAATCAGCTGGCTG	Qy 295 Db 41	
294	GCGGGAAATANACGGGTGCTGGGGAACGCCAGAATGCTGGGTTGGGT	Oy 235	
234	ATGAGTCTGAATACAAGTGGGCTGGGAGCGTCAACGATGCAAATTTCTATCGGCGGTGCG 	Qy 175	
	14 (1-1390) x US-08-851-376A-2 (1-403)	SEQ12-SEQ	
	S. Scordes: 5.54e.176 Langth: 403 2079.00 Marchest 403 2079.00 Marchest Petrop. 403 2079.00 Marchest Petrop. 403 2079.00 Marchest Petrop. 403 2079.00 Marchest Petrop. 403 2079.00 2079.	Alignment Pred. No. Score: Percent S Best Loca Query Mat DB:	

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5.54e-176 2079.00 100.00% 100.00% 82.11%	SIGNA 4 JUT-3 1-68-88-307-3 PORTIN NO. 20235974 ALLION US/888-8207 PORTIN NO. 20235974 PO	183	GCCATGATGGCCGGT	CCCATGGCGGGTGATACCGGCAACGGCAACCTGC 	GTATG	ngagotgaaacgatgacaatgatgggcaaagcac
Length: Matches: Conservative: Nismatches: Indels:	PRESONSE IN PLANTS BY SERVICE TO		ATGGCGGTGATGCCATTAACAATATGG 	ACCTGCAGGCACGCGGTGCCGGT 	GAGCAGTTCAACAAAGCCA 	
403 0 0 0 0	P PERMENT		TOGCACTTGCCAAGCTG	CCGGTGGTTCTTC	GCCAAGGGCATGATCAAAAGG 	CTGAGCAAGCCAGATGAC
			1374		1254 360	1194

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	1194	21 GlydlaGluValLysThrAspAspLySSerTrpAlaLysAlaLeuserLysProAspAsp	Qy 113 Db 32	
	320	GREAGYTCATGGACCAGTAYCCTGAGGTGTTTGGCAAGCCGCAGTACCAGAAGCCGCG GIJGIIII	Oy 107	
		AGCARATTCAACCCCTTTTTCCTTTAAAGCCATACATTCGCCATATGCCAAGAACATTCAACCATATGCCAAGAACATAAAAAAAA	Oy 101 Db 28	
	1014	5 GTGGGTACCGGTATGAAACGGCATTCAGGGCGTGAATATGGGTACGGT 5 GTGGGTACCGGTATGAAACGGGCATTCAGGGCGTGAATATGGGTACGGA 61 ValGlyThrGjyTleGlyWeLLysAlaGlyTleGlnAlaLeunsnaspIleGlyThrHis ;	Oy 95	
	35.4 260	41 GlyGlyLysGlyLeuGlnAsnLeuSerGlyProValAspTyrGlnGlnLeuGlyAsnAla GlyGlyLysGlyLeuGlnAsnAsnLeuSerGlyProValAspTyrGlnGlnLeuGlyAsnAla 2	Oy 89	
	394	35 cdGGGACTGGACGTGGTCAGGCGGTAATSCTGCGACGGTCTTGACGGTTCTTGCTGT 321 GlyGlyLeuGlyGlyGlyGlyGlyGlyAsnAlaGlyThrGlyLeuAspGlySerSerLeu 321 GlyGlyLeuGlyGlyGlyGlyGlyGlyAsnAlaGlyThrGlyLeuAspGlySerSerLeu	Qy 83 Db 22	
	334	73 GABETARTGARGGGTGTGGGGCTGATGGGTAATGGTTGAGGCAGCTCCTTGGGAAC 8 101 GlyValThrAspAlaieuSerGlyLeuMetGlyAsnGlyLeuSerGinLeuieuGlyAsn 2	0y 77 Db 20	
	774	115 CAGGCAGTTCCTTTGGGGCAAGCAGCCGACGCGAGCAGAACGCCTTATAAAAA 7 126 CAGGCAGCAGCAGACGCGAACACGCCTTATAAAAAA 7 127 CAGGCAGCAGCAGACGCGAACACGCCTTATAAAAAA 7 128 CAGGCAGCAGCAGACGCGAACACGCCTTATAAAAAA 7 129 CAGGCAGCAGCAGAACACGCCTTATAAAAAA 7 129 CAGGCAGCAGCAGAACACGCGAACACGCCTTATAAAAAAA 7 129 CAGGCAGCAGCAGACGCGAACACGCGAACACGCCTTATAAAAAAAA	0y 71 Db 18	
	714	5 CTCCTRABAGTCTTCACCGAGTANTCCNAACCCTGTTTGGTGATGGCAAGATGGCACT 5 CTCCTRABAGTCTTCACCGAGTANTCCNAACCCTGTTTGGTGATGGCAAGATGGCACC 6 LeuLeulysMetPheSerGlulleMetGlnSerLeuPheGlyAspGlyGlnAspGlyThr	Qy 65 Db 16	
	160	85 ABGGAGATTCACTTCGGCDAOAATTCCACCTCAGCTCCAGCGACCGAGCGAGTGAGGAG 9	Oy 59	
	40	3 ACCACTTCAACAACTAATTCCCGCTGGACCAGGGGTGGTATTAACTCAACGTCCCAA 3 ACCACTTCAACACAACTACCAA 3 ThrThrSerThrThrAanSerProLeuAapGlnAlaLeuGlyTleAanSerThrSerGin 1	Oy 53 Db 12	
	20	01 AlaLewasnaspketLewGlyGlyserLewasnThrLewGlySerLySGlyGlyasnasn	Oy 47 Db 10	
	00	31 GlyGlyGlyLeuGlyAsnGclyGcgraGcTcAGGTGGCTGGGCGAAGGACTGTCGAC 31 GlyGlyGlyLeuGlyAsnGclyLeuGlyGlySerGlyGlyLeuGlyGluGlyLeuSerAsn 1 31 GlyGlyGlyLeuGlyAsnGlyLeuGlyGlySerGlyGlyLeuGlyGluGlyLeuSerAsn 1	0y 41 Db 8	
	14	S ACCGEZAGARGANGANGAGGACARANGGCGGTGGTGGGGGGTGANGGGGGGTGGGTGAT 	ОУ 35 Въ 6	
	0 4	S. CALCYGGGGCYGGGCGCGCGANTANANGHPACCGTCANTACACYGGCYGGCYGGCYTATT 	0y 29 Db 4	
	0 94	3 GCGGSANTANGGGTTGCTGGGTNCCNGTCCCNANTGCTGGGTTGGGT	Oy 235	
	234	5 ANGAGTYGAANACHAGGGGGGGGGGGGGGGGGGGGAATTYGYRYGGGGGGGG 1	0y 17	
		EQ4 (1-1390) x US-08-984-207-3 (1-403)	SEQ12-SE	
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1195 GACGGAATGACACCAGCCAGTATGGAGCAGTTCAACAAAGCCAAGGGCATGATCAAAAGG 1254

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	gTrpValLeuMetPro 385	380	Db
	GGGTATTGATGCC	1315	Qy.
380	\spThrGlyAsnGlyAsnLeuGln-HisAlaValProValV	361	D.
1314	CCNTGGCGGGTGATACCGGCAACGGCAACCTGCAGGCACGGGTGCCGGTGCTCTTC	1255	9
360	AspClyMetThrProAlaSerMetGluGlnPheAsnLysAlaLysGlyMetTleLysArg	341	B 5
s á	TyGINGIUVALITYSTIITASPASPILYSSETTIPALAUYSALAUHUSETIYSEIOASPASP		9
	GGTCAGGAGGTGAAAACCGATGACAAATCATGGGCAAAAGCCACGGAGCCAGGCCAGATGAC	1135	. 9
320	lnPheMetAspGlnTyrProGluValPheGlyLysProGlnTyrGlnLysGlyPro	301	В
1134	GGTCAGTTCATGGACCAGTATCCTGAGGTGTTTGGCAAGCCGCAGTACCAGAAAGGCCCG	1075	9
300	ArgH18SerSerThrArgSerPheValAsnLysGlyAspargAlaMetAlaLysGluIle	6.1	Db
1074		1015	9
280	valGlyThrGlyIleGlyMetLysalaGlyIleGlnAlaLeuAsnAspIleGlyThrHis	261	DЬ
1014	- 8	955	9
260 .	GlyGlyLysGlyLeuGlnAsnLeuSerGlyProValAspTyrGlnGlnLeuGlyAsnAla	241	Db
954	GTAACGCC	895	9
240	GlyGlyLeuGlyGlyGlyGlyGlyAsnAlaGlyThrGlyLeuAspGlySerSerLeu	221	B
894		835	Q.
220	GlyvalThrAspAlaLeuSerGlyLeuMetGlyAsnGlyLeuSerGlnLeuLeuGlyAsn	201	9
834	SAGTCACTGATGCGCTGTCGGGCCTGATGGGTAATGGTCTGAGCCAGCTCCTTGGCAAC	775	9
200	GlnGlySerSerGlyGlyLysGlnProThrGluGlyGluGlnAsnAlaTyrLysLys	181	망
774	STTCCTCTGGGGGCAAGCAGCCGACCGAAGGCGAGCAGAACGCCTATAAAAAA	715	9
180	LeuLysMetPheSerGluIleMetGlnSerLeuPheGlyAspGlyGlnAspGlyThr	161	용
714	VIGITCAGCGAGATAATGCAAAGCCTGTTTGGTGATGGGCAAGATGGCACC	655	Qy.
160	AsnAspAspSerThrSerGLyThrAspSerThrSerAspSerSerAspProMetGlnGln	141	문
654	ACGACGATTCCACCTCCGGCACAGATTCCACCTCAGACTCCAGCGACCCGATGCAGCAG	595	νΩ
140	ThrSerThrThrAsnSerProLeuAspGlnAlaLeuGly1leAsnSerThrSerGln	121	망
594	CCACTTCAACAACAATTCCCCGCTGGACCAGGCGCTGGGTATTAACTCAACGTCCCAA	535	Ş
120	AlaLeuAsnAspMetLeuGlyGlySerLeuAsnThrLeuGlySerLygGlyGlyAsnAsn	101	Db
534	CGCTGAACGATATGTTAGGCGGTTCGCTGAACACGCTGGGCTCGAAAGGCGGCAACA	475	οy
100	GGGGGTGGTTRAGTRATGGCTTGGGTGGCTCRGGTGGCTTGGGCGGGGGGTGGCTTGGGTGGG	81	B 8
, c	hrGlyWetMetHetMetSerHetGlyGlyGlyGlyLeuwetGlyGlyGlyLeu	0	00
114	->	355	9
50	AlaLeuGlyLeuGlyGlyGlyAsnGlnAsnAspThrValAsnGlnLeuAlaGlyLeuLeu 6	41	Db

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US-08-819-539-3
                                  Query Match:
                                                                            Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                          score:
                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: GOLGMAN, MICHAEL I.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 1460
TELECOMNUTICATION INFORMATION
TELEPHONE: (716) 263-1104
TELEPHONE: (716) 263-1104
TELEPHONE: (716) 263-1104
TELEPHONE: (716) 263-1109
INFORMATION: POR SEQ ID NO. 3
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MEDICINE TYPE: FLORPY GLAS
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GENERAL INFORMATION:
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ARPLICANT: Beer, Steven V.
TITLE OF INVENTION: Hypersensitive Response
TITLE OF INVENTION: Induced Resistance In Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 385 amino acid
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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STREET: Clinton Square, P.O. Box 1051
CTTY: Rochester
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COUNTRY: U.S.A.
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amino acid
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Db	۳	MetSerLeuAsnThrSerGlyLeuGlyAlaSerThrMetGlnIleSerIleGlyGlyAla	ō
οy	235	235 GGCGGAAATAACGGGTTGCTGGGTACCAGTCGCCAGAATGCTGGGTTGGGTGGCAATTCT 294	94
ь	.21	GlyGlyAsnAsnGlyLeuLeuGlyThrSerArgGlnAsnAlaGlyLeuGlyGlyAsnSer 40	0
Qγ	295	295 GCACTGGGGCTGGGCGGGGTAATCAAATGATACCGTCAATCAGCTGGCTG	5
Db	4	AlaLeuGlyLeuGlyGlyAsnGlnAsnAspThrValAsnGlnLeuAlaGlyLeuLeu 60	ő
Qy	355	ACCGGCATGATGATGATGAGCATGATGGGCGGTGGTGGGCTGATGGGCCGTGGCTTA 4	414
Db	61	ThrGlyMetMetMetMetSerMetMetGlyGlyGlyGlyLeuMetGlyGlyGlyLeu 80	ö
V	415	415 GCCGCTGGCTTAGGTAATGGCTTGGGTGGCTCAGGTGGCCTGGGGGGAAGGACTGTCGAAC 474	74

US-08-819-539-3 ; Sequence 3, Application US/08819539

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655 CTGCTGAAGATGTTGAGCGAGATAATGGAAAGCCTGTTTGGTGATGGGCAAGATGGGACC	ANCGACGATTCCACCTCCGGCACAGATTCCACCTCAGACTCCAGCGACCGGATGCAGCAC 	Alamanasphethosdydlysertmaksniihrteudlysertysdlydlyasnass Aconiitaachachacharincoccinsocchsscoccasstriacreanssrccaa Aconiitaachacharincoccinsocchsscoccasstriacreanssrccaasscochallillillillillillillillillillillillilli	GCGGTGACTHAGT MATGCTTGGTTGGTTGACTGCCTGGCCTGAGGCATGTGCAAGGACTTTGCAGGCTGAGGACTTGGTTGG	ACCGGCATGATGATGATGAGCATGATGAGCAGCTGCGCTGGGCTGAATCGGCCCTGGGCTGAATCGGCCCTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT	GCACTEGGGCTGGCTGGCTTACTCAAATGATACCGTCAATCAGCTGGCTTGGCTTACTC	GGCGGAAATAACGGGTTGCTGGGTACCACTCGCCAGAATGCTGGGTTGGGTTGGGAATTCT 	175 ATGACTCTSANTACAAGTGGGCTGGGGGGGTGACAGTGCAAATTCTNTCGCGGGGGGGG 11	Gaps: (1-1390) x PCT-US96-08819-3 (1-385)	Score: Percent Similarity: Best Local Similarity: Query Match:	Alignment Scores: Pred. No.:	STRANDEDNESS: TOPOLOGY: linear MOLECULE TYPE: pro- S96-08819-3	INFORMATION FOR SEQ ID NO. 3: SEQUENCE CHARACTERISTICS: LENGTH: 385 antho acids TYPE: amino acids	REGISTRATION NUMBER: 30,727 REFERENCE/DOCKET NUMBER: 19603/10051 TELECOMMUNICATION: TELECOMMUNICATION: (716) 263-1304 TELECHUNE: (716) 263-1304	APPLICATION NUMBER: US OF APPLICATION NUMBER: US OF APPLICATION TO	APPLICATION NUMBER: FILING DATE: CLASSIFICATION:	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

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REJISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELECHONE: (203)28-1951
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101 AlaleuAsnAspMetLeuGlyGlySerLeuAsnThrLeuGlySerLysGlyGlyAsnAsn
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                                                                                                                                                      GGAGTCACTGATGGGCTGTCGGGGCCTGATGGGTAATGGTCTGAGCCAGCTCCTTGGCAAC
                                                                                                                                                                                                                                    GinGlySerSerGlyGlyLysGinProThroluGlyGluGlnAsnAlaTyrLysLys
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1254 360	195 GACGAANGA-26C,AGCCAGTATGGAGCASTTCAACA-AAGCCAAGGCATGNTCAAGAG 1911		B 63
1194 340	13 GYPCAGGAGGFGAAAACGAGGAGGAAGGAATGAGGAATGAGGAGGAAGGAA		Db Qy
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1074 300	015 AGGCACAGTTCANCCGTTCTTGTGTTATAAGGCATTGGGCGATGGGCAAGGAAGTATCANCCGTTTTGTTTT	_	Db da
1014	55 GTGGGTACCGGTATCGGTATGGAAAGCGGGCATTCAGGCGCTGAATGATATCGGTACGCTACGCTACGCACTCAGACGCTACGGTACGGTACGCTACACGCTACGCTACGCTACGCTACGCTACGCTACGCTACACGCTACACACAC	N 9	Оу
954	895 GGGGGCAAAGGGCTGCAAAACCTGAGAGCGGGCGGTGGACTACCAGCAGTAGGTAACGCC	N 00	Ф

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CACAGGCACAGTTCAACCCGTTCTTTCGTCAATAAAGGCGATCGGGGGAGGGGAAGGGAA 1071	GOCCIOGGENACGGENACGGENATGAAGGGGCATTCAGGGGCGGAATGANTGGGENACG 1011 	CTGGGCGCAAAGGGCTSCAAAACCTGAGCGGGCGGGTGGACTACCACAGTTAGGTAAC 951	AAGGGGGACTGGAGAGCAGGTCATAAGGCTGCCAGGGTCTTGAAGGCTTCGTG 891	AAGGARTAATGARTCGGCTCTGGGCCTAMTGGCTAATGGTCTGAGCCAGCTCCTTGGC 81 AIIII	ACCCAGGCAGTTCCTCTGTGGGGCAAGCAACCCAAGCGAAGCAGACAGA	AlaleuAspCipeTrGcT	ACAATTCACCTCACCACCACCAGCAGCAGCAGCAGCTCCAAAGATCTCACCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	CCCCTGGACCAGGCGCTGGGTATTAACTCAACGTCCCCAAAAGGACGATTCCACCTCCGGGC 615	GGTTLGCTGAACAGCGTCGAAGAGCGGCAACAATACCACTTCAACAACAACTTCC 555 [TGGTTGGTCAGTCAGTGGGCCMGGACTGTGGAAGGCCCTGAACGATATGTTAGGC 4	GATGGGCGGTGGTGGGCTATGGGGGGTAGGCTTAGGCGTGGCTTAGGTAATGGC 43	ANTEANAMENTACCETCAMPCASCTROCTEGCTTACTCACCOCAMPGATGATGATGATGATGATGATGATGATGATGATGATGATG	CARATRCTEGGTTGGCT-GATTCTCCACTGGGCTGGGCGGGGGGT 315	ATSCAAATTTCTAYCGGCGGTGCGGGCGGAAATAACGGGTTGCTGGGTAGCAGTCGC 267 ::: ::: 		Scores: 1,250-25 Length: 338 25.50 Length: 272 25.50 Length: 477 25.50 Length: 477 25.50 Length: 477 25.50 Length: 217 2	STRANDENDESS: TOPOLOGY: Linear MOLECULE TYPE: protein 8-891-234-1

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SEQ12-SEQ4 (1-1390) x US-08-819-539-1 (1-338)
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OY 1199 GACGACGGARGGACCACCACCAGTMOGACCAGCGCAAGGCCAGGGCATGATGAAA 1281 . BD 275 AGGACGGAAGGAACCAGCCAGTMOGACCAGGCCAAGGCCAAGGCCAGGGCATGATGAAA 1281 . BD 275 AGGACGACGAAGCACCAGCCAGTMOGACCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCAAGACGAAGACAAGACGAAGACGAAGACGAAGACGAAGACGAAGACAAGACGAAGACGAAGACAAAAAA

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	LeuAlaAsnAla 338	335	Ъ
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GlyLys 334	SerLeuGlyILeAspAlaAlaValValGlyAspLysIleAlaAsnMetSerLeuGlyLys	315	В
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GlyAla 314	SerAlaValAlaGlyAspThrGlyAsnThrAsnLeuAsnLeuArgGlyAlaGlyGlyAla	295	B
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ProAsp 274	GlyTrpSerSerProLysThrAspAspLysSerTrpAlaLysAlaLeuSerLysProAsp	255	Ъ
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LysAsp 254	<pre>ileGlyGlnPheMetAspGlnTyrProGluTlePheGlyLysProGluTyrGlnLysAsp</pre>	235	8
AAAGGC 1131	ATCGGTCAGTTCATGGACCAGTATCCTGAGGTGTTTGGCAAGCCGCAGTACCAG	1072	Qy
LysGlu 234	HisValAspGlyAsnAsnArgHisPheValAspLysGluAspArgGlyMetAlaLysGlu	215	D)
AAGGAA 1071	CACAGGCACAGTTCAACCCGTTCTTTCGTCAATAAAGGCGATCGGGCGATGGCG	1012	8
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GGTACG 1011	GCCGTGGGTACCGGTATCGGTATGAAAGCGGGCATTCAGGCGCTGAATGATATC	952	δõ
GlyAsn 194	LeuGlyAlaGlyGlyLeuGlnGlyLeuSerGlyAlaGlyAlaFheAsnGlnLeuGlyAsn	175	В
GGTAAC 951	CTGGGCGGCAAAGGGCTGCAAAACCTGAGCGGGCCGGTGGACTACCAGCAGTTA	892	γQ
ProSer 174		168	₽
TCGTCG 891	AACGGGGACTGGGAGGTGGTCAGGGCGGTAATGCTGGCACGGGTCTTGACGGTTCGTCG	832	Qy
Met 167	SerGlyValAsnAsnAlaLeuSerSerIleLeuGlyAsnGlyLeuGlyGlnSerMet	149	Вb
CTTGGC 831	AAAGGAGTCACTGATGGGCTGTCGGGCCTGATGGGTAATGGTCTGAGCCAGCTC	772	29
PheGly 148	LeuAlaAsnSerMetLeuAsnAlaSerGlnMetThrGlnGlyAsnMetAsnAlaPheGly	129	Db
TATAAA 771	ACCCAGGGGAGTTCCTCTGGGGGCAAGCAGCCGACCGAAGGGGAGCAGAACGCCTATAAA	712	5
AsnGln 128	AlaLeuAspAspLeuLeuGlyHisAspThrValThrLysLeuThrAsnGlnSerAsnG	109	В
GATGGC 711	ATAATGCAAAGCCTGTTTGGTGATGGCCAAGATGGC	676	δÃ
AspLys 108	GlyAspAlaLeuSerLysMetPheAspLys	99	₽
AGCGAG 675	ACAGATTCCACCTCAGACTCCAGCGACCCGATGCAGCAGCTGCTGAAGATGTTC	616	Qy
SerGLy 98		97	DЪ
CTCCGGC 615	CCGCTGGACCAGGCGCTGGGTATTAACTCAACGTCCCAAAAACGACGATTCCACCTCCGGC	556	40
oLys 96	AsnGlyAlaGinGlyAlaSerAsnLeuLeuSerValProLys	83	Db
MATTCC 555	GGTTCGCTGAACACGCTGGGCTCGAAAGGCGGCAACAATACCACTTCAACAACAAATTCC	496	Qy
rPheGLy 82	LeuGlyAlaSerSerLySGlyLeuGlyMetSerAsnGlnLeuGlyGlnSerPheGly	04	Db

Search completed: January 14, 2003, 17:19:34 Job time : 22.5 secs



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HrpN.	
HRPN.	
Erwinia stewartii.	artii.
Bacteria; Pr	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Pantoea.	
NCBI_TaxID=66271;	6271)
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SEQUENCE FROM N.A.	M.A.
STRAIN-SS104;	
Frederick R.	Frederick R.D., Ahmad M., Majerczak D.R., Arroyo-Rodriguez A.S.,
Manulis S., Coplin D.L.;	coplin D.L.;
"Genetic org	"Genetic organization of the Pantoea stewartil subsp. stewartil hrp
gene cluster	gene cluster and sequence analysis of the hrpA, hrpC, hrpN and wtsE
operons.";	
Submitted (J	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF2828	EMBL; AF282857; AAG01466.1;
SEQUENCE 3	382 AA; 37878 MW; 8BA8C723F2DA38BB CRC64;

Alighment Scores: 5.33e-75 Length: 382 Score: 5.31e-75 Matches: 21 Score: 5.31e-17; Matches: 21 Score: 5.21A Mascretive: 44 Secretive: 64 Secr	09 1132 COGGGTCAGAGGGTAAAACGATGACAAATGATGGGCAAAATGATGAGGAAAAGCAAATGATGAGGAAAAGCAAATGATGAGGAAAAGCAAATGATGAGGAAAAGCAAAATGATGAGGAAAAGCAAAATGATGAGGAAAAGCAAAATGATGAGGAAAATGATGAGGAAAATGATGAGGAAAATGATG
TOAGTOTGAATACAACTTGGGCTGGGACGATGGAACTTTCTATCGGCGG	Oy 1252 AGGCCATGGCGGTGATACCGGCAACCTGCAGGCACGGGGGGGG
GGCGGAAAFAACGGGTTGGTBGGTRCCAGTCGCCAGAATGCTGGGTTGGGTGGAATTCT	Oy 1312 TOSCTOSGTANTGANTGCONTGATGGCOCGTGATGCCATTAACAATATGGCACTTGGCAAG 1371
GlyGlyAshAshGlyLeuMetGlyThrAspLeuArgThrAspClyLeuGlyLeuLeuSer	1372 C7000GCGCGCT 1383
295 GCACTGGGGCTGGGCGGGGTANTCAAATGATGCGTCAATCAACTGGCTTGGCTTA 351	179
352 CTCACCGGCATGATGATGATGATGATGATGGGGGGTGGTGGGGCTGATGGGGGGTGGC 411	RESULT 2 OSKH45 ID OSKH45 AC OSKH45 PRELIMINARY; PRT; 365 AA.
	OT 01-007-2000 (TYEMBLEA: 15, Greated) DT 01-007-2000 (TYEMBLEA: 15, Greated) DT 01-MAR-2000 (TYEMBLEA: 20, Last sequence update) DF Harpla: 002 (TYEMBLEA: 20, Last annotation update) DE Harpla:
472 AACGGGTGAACSATATGTTAGGGGGTGGGTGGAAAGGGGGGAAC 531	OS Pantosa agglomerans pv. gypsophilae. OC Bacteria, Proteobacteria, gamma subdivision: Enterobacteriaceae; OC Pantosa.
532 AATACCACTTCAACAACAAATTCCCCGCTGGACCAGGCGCTGGGTATTAACTCAACGTCC 591	OX N.HTXX.LD-48986; RN [1] RP SEQUENCE FROM N.A. RX MEDIANS-21171042; PubMed=11277443;
592 CAMAACGACARTYCCACCTCCGGCACAGATTCCACCTCAGCGACCGGACCCGATCCAC 651 124 ThrGlyAspAspSerLeuSerCyAlaGclyGinThrSorGlyMetSerProtection 142	RA MOE H., Manulis S., Zook M., Nizan R., Coplin D.L., Barzah I.; RT "Genetic organization of the hrp gene cluster and dspAE/AF operon in RT erwinia herbicola pv. gypsophilae."; RL Mol. Plant Microbe interact. 14:331-436 (2001).
652 CARCTECTBANANOTICNAGGAGATATICCABAGCCTECTTGGTTGGTGATGGGCAAGATGGC 711 [11]	QUENCE 365 AA; 36784 NW; 6F79BB6DDD95AC2A
712 ACCAGGCAGTTCCTTGGGGGCAACGCAAAGCCGAGCCGA	Price: NU: 0.08 03 Manighth: 300 Price: NU: 0.08 03 Manighth: 224 Pricent Similarity: 07.51% Conservative: 42 Past Local Similarity: 56.85% Mismatches: 90
772 AAAGAAFDACTGANGGGTTGGGGCTGATGGGTANTGGTCTGAGCGAGCTGCTTGGC 831 181 LUHHHHHHHHHHHH::::HHH 181 LY9GIYVAlThrAspAlaLeuThrAlaPheMcGJJyGJJyeuJsetClaVallaGJy 200	Gaps:
892 ANCEGEGALTROGARGETGETCHEGEGEGEGTARTGCTTGGCACGGGTCTTGACGGTTCGTCG 891 201 ASHGLYSETGLUGLYGLY-LBURGTYMETGLYLBURGLYGLYGLYSENGLY 218	Oy 175 ATGASTCTGAATACAACGGGCTGAGAGCTCAACGATGCAAATTTCTATCGGGGGTGCG 234 [
892 CTGGGGGGAAAGGCTGCAAAACCTGACGGGCCGGTGGACTACCACCACTACGTAAC 951 219 Leodyyd Ywyd Araeth Charlen y Hilli Hil	QY 235 GGCGGAAATAACGGGTTGGGTGGGTACCAGTCGCCAGAATGCTGGGTTGGGTGGCAGATTCT 294 III ::::IIIIIIII
952 GCCGTGGGTACCGGTATCGGTATGAAAGCGGCGGATCAGGCGCTGAATGATATCGGTACG 1011 239 AlaTiGGJTTATCJYVALCJyWGLGJYAGAGCTGGLAATGAATAATGTTATC 258 239 AlaTiGGJTTATCJYVALCJyWGLGJYAGAGGTGGLAATGAAAASTIJGGJTTATC 258	CTTACTC
1012 CACAGGCACAGTTCAACCCGTTCTTTCGTCAATAAGGCAATGGGGGGATGGCGAAGGAA 1071 259 WISSETAAppSeSGTThATGSGETPÄNTAGSGTTAATGAGTTAAGAGTAAGAAAAGAATAAGGTA 278	Qy 355 ACCGGCATGATGATGATGATGATGATGATGAGGGGTGGTGGGGTGGGTGGGTGGGTTGGCTTA 414 Db 53 ThrAlametheredbecterkamethericty(1)587GC1/yearCalyGlyGlyber 71
1072 ATGGTGGGTGATGGAGCAGTATCCTGAGGTGTTTGGGAGCGGGATTACCAGAAAGGC 1131 279 VAIGIYGIAPHeWelhagGlmTyrFroGluThrPheGlyLysProGlnTyrGInLysAsn 298	Qy 411 GGCGGTGCCTTAAGGAATGGCTTGGGTGGCTCAGGTGCCTGGCCGAGGGCTG 46(G

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1182	CAGAAAGGCCCGGGTCAGGAGGTGAAAACCGATGACAAATCATGGGGCAAAAGCACTGAGC	1123	20
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846	GCGCTGTCGGGCCTGATGGGTAATGGTCTGAGCCAGCTCCTTGGCAACGGGGGACTGGGA	787	Q.
1159	AsnGlyGlyThrGlyGlyThrGlyGlyThrGlyGlyThrGlyGlyLySGlyGlyMetGly	1140	DЬ
786	TETTGGGGGCAAGCAGCCGACCGAAGGGGAGCAGAACGCCTATAAAAAAAGGAGTCACTGAT	727	9
1139	GlyAlaGlyGlySerGlyGlyAlaAsnPhe	1130	Db
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1129	GlyGlyThrGlyGlyThrGl	1120	Db
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1077	7 GCGATGGCGAAGGAAATCGGT	105	Q
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1056	AATGATATCGGTACGCACAGGCACAGTTCAACCCGTTCTTTCGTCAATAAAGGCGATCG	997	9
365	6 AlaAlaGlyGlyAspGlyGlyAlaGlyGlyAsnGlyGlyAlaGlyGlyAsnGlyGlyVal	346	Db
996	CAGTTAGGTAACGCCGTGGGTACCGGTATCGGTATGAAAGCGGGCATTCAGGCGCTG	940	Qy
345	7 AlaGlyGlyAlaGlyGlyAlaGlyAlaThrGlyIleAsnGlyProAlaGlyIleSer	327	Db
939	GACGGTTCGTCGCTGGGCGGCAAAGGGCTGCAAAACCTGAGCGGGCCGGTGGACTACCAG	880	9
326	7 LeuGlyAsnGlyGlyAlaGlyGlyValGlyGlyAlaGlyGlyAlaGlyAlaGlyAla	30	Db
879	CTTGGCAACGGGGACTGGGAGGTGGTCAGGGCGGTAATGCTGGCACGGGTCTT	826	Qy
306	GlyGlyValGlyGlyAsnGlyGlyArgGlyGlyTrpLeu	294	Db
825	AAAGGAGTCACTGATGCGCTGTCGGGCCTGATGGGTAATGGTCTGAGCCAGCTC	772	ρ
293	SerAspGlyGlyAspGlyGlyAla	286	Db
771	ACCCAGGGCAGTTCCTCTGGGGGCAAGCAGCCGAACCGAAGGCGAGCAGAACGCCTATAAA	712	δδ
285		280	D
711	CAGCTGCTGAAGATGTTCAGCGAGATAATGCAAAGCCTGTTTGGTGATGGGCAAGATGGC	652	Qy
279	ProGlyGlnAspGlyAlaAlaGlyValAlaGlySerAspAspGlyAlaGly	263	рь
651	CAAAACGACGATTCCACCTCCGGCACAGATTCCACCTCAGACTCCAGCGAGCCGATGCAG	592	9
262	GlyValGlyGlyValGlyAlaAlaGlyAlaAsnGlyAlaThr	249	Db
591	AATACCACTTCAACAACAAATTCCCCGCTGGACCAGGGCTGGGTATTAACTCAACGTCC	532	γg
248	GlyAlaGlyGlyAsnAlaGlyTrpPheGlyHisGlyGlyAlaGly	234	망
53I		473	Qy
233	AlaGlyLeuPheGlyAsnGlyGlyAlaGlyGlyAlaGlyGlyAlaGlyGlyGlyAlaGly	214	Db
471	0	433	νQ
213	GlyGlyGlyWalGlyGlyMetGlyGlyAlaGlyGlyGlyAlaGlyGlyAlaGlyGlyAsn	194	Db
432	ATGAGCATGATGGGCGGTGGTGGGTGATGGGCGGTGGCTTAGGCGGTGGCTTAGGTAAT	373	οy
193	GlyThrGlyGlyThrGlyGlyTrpLeuAlaGly	183	Db
372		313	ç,
182	PheGlyIleGlyGlyAlaGlyGlyAlaGlyGlyAlaGlyAlaProGly	167	Db
312	CTGGGTACCAGTCGCCAGAATGCTGGGTTGGGTTGGCAATTCTGCACTGGGGCTGGGCGGC	253	Qγ
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252	GGGCTGGGAGCGTCAACGATGCAAATTTCTATCGGCGGTGCGGGGGGGAAATAACGGGTTG		Ŷ
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400 ATGGGCGTGCTTAGGCGGTGGCTTAGGTAATGGCTTGGGTGGCTC	Ωγ
340 CTGCCTGCCTTACTCACCGCATGANGANGANGANGANGANGANGANGANGANGANGANGANG	B 9
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GTGGCAATTCTGCACTGGGGCT	Qy
226 GGCGTCCGGGCGAANAACGGTTGCTGGGTACCACTGCCCACAATGGCCACAATGGCCACAATGGCCACAATGGCCACAATGGCCACAATGGCCACAATGGCCACAATGGCCACAATGGCTGCACAATGGCCACAATGGCCACAATGGCCACAATGACAATGGCTGCACAATGGCCACAATGACAATGGCCACAATGAATG	Оy
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487 IleAlaGluGlyEeuThrLeuGluLeuGlyGlyAspGlyGlyGluGlyGly	
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346 GGCTTACTCAGCCATCATGATGATGATGATGATGATGAGTGAG	Db 99
/ 298 CHGGGGGGGGGGCGGTMATCAMAATGATACGTCAMTCAGCTGGCTGGCTGGGGGGGGGG	Db Qy
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193 GGGCTGGGA ::: 359 GlyIleGln	Db Oy
/ 133 CTCGCGAGGTACGTTGAATTCATAGAGGAATAGGTTAATAGAGCTGAATAGAGTGAATAGAGTTAATAGAGTGAATAGAGTTAATAGAGTGAATAGAGAGAGAGAATAG	Db Oy
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970 GGTATGAAAGCGGGCATTCAGGCGCTGAATGATATCGGTACGCACAGGCACAGTTCAACC	ACC 1029	
724 GlyGlyAspGlyGlyAlaGlyGlyAlaGlyGlyAsnAlaGlyGlyAsnAlaGlyGlyAlaGly	aGly 743	
1030 CGTTCTTTCGTCAATAAAGGCGATCGGGCGATGGCGAAGGAAATCGGTCA	AGTT 1082	
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1083 CATGGAGCAGTATCCTGAGGTGTTTTGGCAAGCCGCAGTACCAGAAAGGCCCGGGTCA	AGGA 1142	
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1143 GGTGAAAACCGATGACAAATCATGGGCAAAAGCACTGAGCAAGCCAGATGACGAAT	SAAT 1202	
781 GlyAspGlySerGly TySGlyGlyGlyGlyGlySerGly	rGly 792	
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793 GlyThrGlyGlySerGlyAlaProTleGlyGlyGlyAlaGlyGlyThrGlyGlySerGly	rGly 812	
1239 GGCATGATCAAAAG	1253	
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1254GCCCATGGCGGGTGATACCGGCAACGGCAACCTGCAGGCACG	3CGG 1298	
833 ProGlyAsnGlyGlyAsn-AlaGlyAspGlyGlyAsnGlyGlyAsnAlaGlyAlaGlyGl	lyG1 852	
1299 TGCCGGTGGTTCTTCGCTGGGTATTGATGCCATGATGCCGGTGATGCCATTAACAA	NTAT 1358	
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ALIGNMENTS

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Wei 2M., Lai	Wei 2M., Laby R.J., Zumoff C.H., Bauer D.W., He S.Y., Collmer A.,	
Beer S.V.;		
"Harpin, elic.	"Harpin, elicitor of the hypersensitive response produced by the	

plant pathogen Erwinia amylovora."; Science 257:85-88(1992).

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              AGGCACAGTTCAACCCGTTCTTTCGTCAATAAAGGCGATCGGGCGATGGCGAAGGAAATC 1074
                                                                                                                                            GlyGlyLysGlyLeuGlnAsnLeuSerGlyProValAspTyrGlnGlnLeuGlyAsnAla
                                                                                                                                                                                                                 GGGGGTGGCTTAGGTAATGGCTTGGGTGGCTCAGGTGGCCTGGGGGAAGGACTGTCGAAC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaLeuGlyLeuGlyGlyAsnGlnAsnAspThrValAsnGlnLeuAlaGlyLeuLeu
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SerAspSerSerThrArgSerPheValAsnLysGlyAspArgAlaMetAlaLysGluIle
                                                                    ValGlyThrGlyIleGlyMetLysAlaGlyIleGlnAlaLeuAsnAspIleGlyThrHis
                                                                                                            GTGGGTACCGGTATCGGTATGAAAGCGGGCATTCAGGCGCTGAATGATATCGGTACGCAC 1014
                                                                                                                                                                                GGCGGCANAGGGCTGCAAAACCTGAGCGGGCCGGTGGACTACCAGCAGTTAGGTAACGCC 954
                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuLeulysMetPheSerGluIleMetGlnSerLeuPheGlyAspGlyGlnAspGlyThr 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCTGANGATGTTCAGCGAGATAATGCAAAGCCTGTTTGGTGATGGGCAAGATGGCACC 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGCTGAACGATATGTTAGGCGGTTCGCTGAACACGCTGGGCTCGAAAAGGCGGCAACAAT 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyGlyLeuGlyAsnGlyLeuGlyGlySerGlyGlyLeuGlyGluGlyLeuSerAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyGlyAsnAsnGlyLeuLeuGlyThrSerArgGlnAsnAlaGlyLeuGlyGlyAsnSer
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SEMPLEMENT AND SECRETION SECRETORS VIA THE HEP SECRETION PATRAMA.
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15-DEC-1998 (Rel. 37, Last annotation update)
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                                                                                                                                                                                                                    EMBL: L78834; AAB49733.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harpin (Harpin-ECC) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
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SEQ12-SEQ4

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1180 AGCAAGCCAGATGACGGAATGACACCAGCCAGTATGGAGCAGTTCAACAAAGCCAAG 1239	1120 PRCSGAMAGGCCGGGGGGGGGGGGGGAAGCGATGAMACCGATGAAGAATGANGGCGCAAAGCACTG 1179 270 TyrGlnLyssAspAsnTrpGlnThrAlaLysGlnG::411111111111111111111111111111111111	1060 APGGCGAAGAARCGGCAGTCANGACCACRACCGAGGGGTTCCCAAGCCCGG 1119 250 MCLAlalysGlutleGlyGlnPheMcLAspGlnTyrProGluValPheGlyLysAlaGiu 269	230 AsnīleSerThrHisAsnAspSerProThrArgTyrPhevalAspLys61uAspArgGly 249	940 CANTIFACETANCECCOTGGGTACCCGTANTGAAACGGGCATTCAGCGCCTAAAT 999 910 CANTIFACETANCECCGTGGGTACCCGTATGAACGGGCATTCAGCGCCTAAAT 999 910 CANTIFACETANCECCATGGGTACCGTATGAGCGGCATTCAGCGCTAAAT 999 910 CANTIFACETANCECTAACGTAACGTATGCTAACGTATGCTAACGTATGCTAACGTATGCTAACGTAACGTATGCTAACGTAACGTATGCTAACGTAACACGTAACACGTAACACGTAACACGTAACACACAC	880 CACGGTTGGTCGGTGGGCGGAAGGGCTGGAACGGGCGGGGGGGG	82 CHACIA, TOLAMANONUMATIONOMOMINITATION CONTROL TOLAMANOLITE 873 184 GINTHILYSCIYGIN	To enactivities and enaction to the control of the	700 GGUZAAAANGCACCCAAGGGAATTCTTTGGGGUAAAGGACCCGACCGAAGGACGAACGAA 799 144 GlyMatserolnolnolnolnolnolnolnolnolnolnolnolnolno	640 GACCCGATGCAGCAGCTGCTGAAGATTCAGCGAGATTCATTC	580 AACTOMOGTICCAMANGAGANTICCACCTCGGGAAATTCGACCTCAGACTCGAGC 639 119 GlymethanalamethanProseralametheuGlyser	520 AAAGCGGCAACAATACCACTTCAACAACAAATTCCCCCCGGTGGACCCGTGGGCGGTGGGCGGTGGGGGG	460 GANGANTOTICGHANGCKTRANGCKTTHAGCGGTTCCCTGNANCACGCTGGGGTCG 519	418	358 GGC:rphrightantantanchersnegggcrigercggcrightegggcrightegg 417 57 Thrwetwetchewetciys: Hill	298 CTGGGGCTGGGCGATATCAAATCAATACCGTCAATCAGCTGGCTG	241 AATAACGGGTTGCTGGGTACCAGTCGCGAGAATGCTGGGTTGGGT	181 CTGAMTACAAGTGGGCTGGGAGCGTCAACGATGCAAATTTCTATCGGCGGTGCGGGCGG	SEQ4 (1-1390) x HRPN_EEWCA (1-356)
Qy 316 AATCAAAATGATACCGTCAATCAGCTGGCTTACTCACCGGCATGATGATGATGATG 375	Oy 268 CAGAMECTOGETTGGGTGGG-AATTCTCGA	Oy 211 ANGLANATICHAY:GGCGGTGGCGGGGGAPAHGGGGTTGCTGGTGCATGGC 267 LILLI LIL		718.50 milarity: 52.72% Similarity: 42.57% h: 28.38%	Length:		modified and this entitles requires or send an email t		CC -1- FUNCTION: ELICIT'S THE PRESENSITIVE RESPONSE (HE) IN THE PLANT CC UPON IMPECTION: HANDE HELCIT'S HE IN NON-HOSTE'S AND IS ALSO CC REQUIRED FOR PATHOGREFICTY IN HOST PLANTS. CC REQUIRED FOR PATHOGREFICTY IN HOST PLANTS. CC -5- SUBJECTIONAL DICATIONAL SCERETICS IN A THE HER DESCRIPTION PATHWAY.				pr 0.760v-1997 (Rel. 35. Last seguence update) pr 15.780c-1997 (Rel. 37. Last seguence update) pr 15.780c-1998 (Rel. 37. Last annotation update) pr Harpin (Harpin-ECN). ON MERNA	23	É	Oy 130 GCGGGGGGTTTGGTGGGGATANGGCGGGATAGGGGGGATAGGGGATAGGATA	dy 140 Ultillillillillillillillillillillillillil	

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teria: Proteobacteria: gamma subdivision: Enterobacteriaceae:
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- 6	72 CTGGGGGGGGGT 1383
1371	1312 TCGCTGGGTATTGATGCCATGATGGCCGGTGATGCCATTAACAATATGGCACTTGGCAAG
1311	1252 AGGCCATGGGGGTANTACGGCAACGGCAGCTGCAGGCAGCGGTGCCGGTGCTGGTGTTCT 1257 AGGCCATGGGGTTCT
1251 296	1192 GAGRACGRANTRIACACCAGCOAGTATGAGRACTETTCAACAGCAAGGCATGCTAGAAAA 11194 AAGAACAAAA 11194 AAGAACAACAACAAGAACAACAACAACAACAACAACAACA
1191 276	1132 CCGGGTCAGAGGGTCAAACCGATGACAAATCATGGGCAAAGCAACGAACG
1131 256	1072 AFGGGTAATTANTGAACAAFACCTBAGTGTTTGGCAAGCGGCAGTACCAAAAGGG 11111111111111111111111111111
1071 236	1012 CARAGGARAGHTCAACCGTTCTTTCGTCAATAAAGGGARTGGGGAAGTGGCGAAGT 1012 CARAGGARAGHTCAACCGTTCTTTCGTCAATAAAGGGARTGGCGAAGTGGCGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG
216	
951 196	892 CTGGGGGGCAAAGGGCTGCAAACCTGAACCGGGCGGGTGGACTGACAGCAGTAAGTA
891 176	832 AACGGGGGACTGGGAGGTGGTCAGGGCGGTAATGCTGGCACGGCTTGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTGGAGGGAG
169	772 AAAGGACTAACTGARGGCCTGCGCGCCTGARGGGFAYGGCTGACCCACCTCGTTGGC
771 150	AGCCGACCGAAGGCGAGCAGAACGCCTATAAA
711	GATGGGCAAGATGGC ::: H1sAspThrValThrLysLeuThrAsnGlnSerAsnGln
675 110	GACTCCAGCGACCCGATGCAGCAGCTGCTGAAGATGTTCAGCGAG
100	ATTCCACCTCCGGC
98	6 GGTTCGCTGAACACGCTGGGCTCGAAAGGCGGCAACAATACGACTTCAACAACAAATTCC ::::: ::: 5 Agn
495	436 TROOTGGCTCAGCTGGCCTGGGGAAGGAATTGGAAGGCCCTGAACGATATGTTAGGC 436 TROOTGGCTCAGCATATGTTAGGCCGGGGGGGGGGGGGGGGG
435	GGCTTAGGCGGTGGCTTAGGTAATGGC
57	41 LysieuSerSerThrIleAspLysieuThrSerAlaLeuThrSerMetMet

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RESULT 4

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Query Match:
DB:
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Enkaryota: Viridaplantae: Chlorophyta: Chlorophyceae: Volvocales:
Chlamydomonadaceee: Chlamydomonas.
MCBLTMAXD-9052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL PRINCIPALINA SECURINCE FROM N.A.

MEDILES-5017362; Debmed-1599252;

MEDILES-5017362; Debmed-1599252;

MEDILES-5017362; Debmed-1599263;

MEDILES-5017362; Debmed-1599263;

MEDILES-5017362; Debmed-159926;

MEDILES-5017362; Deb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Glycosylated polyproline II rods-with-Kinks as a structural motification hydroxyproline rite bytcoproteins.";
Blochemistry 40:2978-2887(2001).
                                                                                                                                                                                                                                                                                        29
40 339
9 279
9 399
455
455
54219 MW;
                                   7.94e-13
316.50
34.11%
29.93%
12.21%
                                                                                                                                                                                                                                                                                                                                                      VEGENATUE CELL MALL PROTEIN GP1.
49 X 5 AN APPROXIMATE PREPAR REPEATS.
POLY-PRO (GLONG. ) (POTENTIAL).
N-LINED (GLONG. ) (POTENTIAL).
N-LINED (GLONG. ) (FOTENTIAL).
N-LINED (GLONG. ) (FOTENTIAL).
NA: ASSA (94) 455 (025 (25 CEC64)).
                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
129
142
142
142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
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SEQ12-SEQ4 (1-1390) x GP1_CHIRE (1-555)

9 8 20 Db 9 Вb ç 망 Q D 8 B Q g Š Db Š D Š B õ 망 9 B 9 Db 9 밁 Ş B 8 밁 ô 맖 9

8

337 LeuAlaAsnAla 340

5

B 9 B 9 B

	EATCATCATGCCGGTGAGTAAGCCAGCCAGC 339	8 AGCCCACCACCGCCCATCATGCTCATCAT	39
ω υ	TGAGCCACCCAAGCCATTACCTAAGCCACGCCTAAGCCACCGCCATC 399 	8 CCCAGGCCACC	25 6
	roValProProSerProAlaProProSer 253	4 CCTAACATATCGTTCAĞ ::: 4 ProSerProSerProPr	234
w 01	GCCCAGC	4 GAATTTGTTGTTGAAGTGGTATTGTTGCCGGCCTTTCGF 5	22
- 0.	GTTAATACCAGCGCCTGGTCCAGCGGG 555	CCGGAGGTGGAATCGTC	212
	AGCTGCTGCATCGGGTCGCTGGAGTCTGAGGTGGAATCTGTG 615	TCGCTGAACATCTTCAG	205
_ ,	SOCCATCACCAAACAGGCTTTGCATTATC 675	CCCCCAGAGGAACTGCCC	191
	TTCG		782 176
	ATTACCCATCAGGCCCGACAGCGCATCA 783		156
y	ACCGCCCTGACCACCTCCC 843 ProProSerProAlaProProSerPro 155	AGCGACGAACCGTCAAC	136
	ProSeri	GCGTTACCTA	953 120
	CGCTTTCATACCGATACCGGTACCCACG 954	3 TGCGTACCGATATCATTCAGCGCCTGAATGCC	1013
	CGGGTTGAACTGTGCCTG 101	ATTTCCTTCGCCATCGCCGATCGCCTTT	1073
	CACCTCAGGATACTGGTCCATGAACTGACCG 1074	3 GGGCCTTTCTGGTACTGCGGCTTGCCAAACAC 	81
4	TTTGTCATCGGTTTTCACCTCCTGACCC 1134	TCATCTGGCTTGGTCAGTGGTTTTTGCCGA	1193
	ATACTG	CTTTTGATCATGCCCTTGGCTTTG	1253
۵	GCAGGTTGCCGGTATCACCCGCCATGGGC 1254	GCACCGCGTGCCT	1301
2	CCCAGCGAAGAACGACG 1302 apheasnCysProProSerProAlaProPro 46	ATAAlaAsnAlaGlnCysValProGlyGlyI	1322

9 DЬ Ş 9 8 õ 망 õ Ş 문 용 S õ D_p 문 δ 8 õ 8 8

202

Alignment Scores:
Pred. No.:
Score:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

6.69e-09 254.00 34.13% 27.16% 9.80%

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

113 129 150 124 20 SIGNAL CHAIN REPEAT REPEAT DOMAIN REPEAT DOMAIN DOMAIN

1 20 21 620 10 73 148 151 229 242 229 235 236 242 205 620 499 600 620 AA; 65406

SEQUENCE

WW;

CONTAINS THE SER-PRO(4) REPEATS.
3 X APPROXIMATE TANDEM REPEATS.
; 64LDD2278AB28524 CRC64;

EMBL; X13885; CAA32090.1; -.
PIR; S06733; S06733.
Repeat; Cell wall; Glycoprote
Rydroxylation.

Glycoprotein; Signal; Structural protein;

POTENTIAL.
EXTENSIN.
H-A-P-P.
H-A-P-P.
2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.

338 повтионостительностительного посторого податажение податажение до 279
VACCEGITATITECGCCEGCA
305 ProproSerProSerProProSerProValProProSerPro 318
218 ATTTGCATCGTTGACGCTCCCAGGCCA 192
319 AlaproValProProSerProAlaPro 327
TODAC
EXTN_TOBAC STANDARD; PRT; 620 AA. Pl3983:
01-JAN-1990 (Rel. 13, Created)
16-CCT-2001 (Rel. 40, Last annotation update)
HRGPNT3.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
I_TaxID=4097;
SEQUENCE FROM N.A.
STRAIN-CV. Xanthi: TISSUE-Leaf;
REDLINE=90128263; Funned=2012909; Relier B., Lamb C.J.;
"Specific expression of a novel cell wall hydroxyproline-rich
<pre>glycoprotein gene in lateral root initiation."; Genes Dev. 3:1639-1646(1989).</pre>
"HE MECHANICAL DENETRATION OF THE COSTEX AND EPIDERMIS OF THE
CALLOGO
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or send an email to license@isb-sib.ch).
(

2-SEQ4	24 (1-1390) x EXTN_TOBAC (1-620)	
1339	3 CGSCCATCATGGCATCAATACCCAGGGAAGAACCACCGGGACGGGGGGGCCTGCAGGTTGC 128	3 80
1279	OGTTGCCGGTNTCACCCGCCATGGGCCTTTTGATCATGCCCTTGGCTTTGTTGAACTGCT 122	20
244	Hisginpro 246	on
1219 247	215 CONTACTGGCTGGTGTCATTCCGTCGTCATGCTCAGTGCTGTTGGCCATGATT 116	50
1159	TGTCATCGGTTTTCACCTCCTGACCCGGGCCTTTCTGGTACTGCGGCCTACCAAACACCT 1100	90
262	ProproThrTyrSerProproProPro	on
1099	CAGGATACTGGTCCATGAACTGACCGATTCCTTCCCCATCGCCC 105	
277	GinerosererornriyesereroproproproThrTyrsereroproproproserero 296	0
1054	GNTCGCCTTTATTGACGAAAGAACGGGTTGAACTGTGCCTGTGCGTACCGATATCATTCA 995	, ,
200		
300	ProProProproAlaTyrSerProSerProProProProThrProThrPhe 317	-
934	AGTCCACCGGCCCGCTCAGGTTTTGCAGCCCTTTGCCGCCCAGGG 890	
318	SerProProProProAlaTyrSerProProProThrTyrSerProProProProThrT 337	7
337	889 ACGAACCGTCAAGACCCGTGCCAGCATTACCGCCCTGAC 851	~ -
850 357	CACCTCCCAGTCCCCCGTTGCCAAGGAGCTGGCTCAGACCATTACCCATCAGGC 797	
796	GCGACAGCGCATCAGTGACTCCTTTTTTAFAGGCGTTCTGCTCGCCTCGGCTCGG	~
377	roProProProSerPheSerPro	2
736	**************************************	~
392	erProProProProAlaTyrSerProProLeuProAlaProProThrTyr 409	
676	TETEGETGAACATETTCAGCAGCTGCTGCATCGGGTCGCTGGAGTCTGAGGTGGAATCTG 617	
910	SerproproproThrTyrSerP 418	
418	TUCKORKOTGRANTGENEGENEGENEGTYSAGTYRATACCCAGCCCTGRGYCCACCG 557 IIII IIIII IIIIIIIIIIIIIIIIIIIIIII	
556	GGGAATTTGTTGTTGAAGTGGTATTGTTGCCGCCCTTTCGAGCCCAGCGTGTTCAGCGAAC 497	7
135	ProproProproProproAlaTyrSerprop 443	
496	CGCCTAACATATCGTTCAGC	
469	169 ACAGTCCTTCGCCCAGGCCACCTGAGCCACCCAAGCCATTACCTAAGCCACCCC 416	
415	CTAAGCCACOGCCCATCAGCCCACCAGCCCATCATCATCATCATCATCATCATCATGCCGG	
483	roProSerProIleTvrSerProProProPro	

B 0 B 0 B 0 B 0 B 0

434 GlyThrGlyLe	OY 982 GGCATTCAGGCGCTGAATGATATCGGT 1008	Oy 922 GGGCCGGTGGACTACCAGCAGTTAGGTAACGCCGTGGGTACCGGTATCGGTATGÄAAGCG 981	Db 405 AsnGlyGlyAsnGlyGlyAsp	Qy 852 ANTGCTGGCACGGGTCTTGACGGTTCGTCGCTGGGCGCAAAGGGCTGCAAAACCTGAGC 921	pb 385 GlyGlyThrGlyGlyAspGlyGlyAsnGlyGlyLeuGlyAlaGlySerGlyAlaLysGly 404	QY 820 CAGCTCCTTGGCAACGGGGACTGGGAGGTGGTCAGGGCGGT 861	MG1yG1yAlaG1yG1ySerG1yG1yThrA	Qy 760 AACGCCTATAAAAAAGGGGTCACTGATGCGCTGTCGGGGCCTGATGGGTAATGGTCTGAGC 819 :::	DD 343 GIYGIYTHEGIYGIYGIYGIYHHEGIYGIYGIYHIFGIYGIYASHGIYGIXASHGIY 364		727 TOTGGGGGGAAGGAAGGAGGGAAGGAAGGAAGGAAGGAAG	Db 327AlaLysLeuPheGlyAspGlyGlyAlaGlyGlyAlaGlyGlyMetGlySerThr 344	QY 676 ATAATGCAAAGCCTGTTTGGTGATGGGCAAGATGGCACCCAGGGCAGTTCC 726	Db 319 AsnGlyGlyHisGlyGlySerAla	Qy 616 ACAGATTCCACCTCAGACTCCAGCGACCCGATGCAGCTGCTGAAGATGTTCAGCGAG 675	DD 302 GLylleAspProGlyAsnGlyGlyGlnGlyAtaAspThrGlyAsnAlaGly 318	:::	こので、このでは、このでは、このでは、このでは、このでは、このでは、このでは、こ	:::	Oy 496 GGTTCGCTGAACACGCTGGGCTCGAAAGGCCGGCAACAATACCACTTCAACAAAATTCC 555	Db 277 LeuSerGlyAsnGlyGlyThrGlyGlyGly	Qy 436 TTGGGTGGCTCAGGTGGCCTGGGCGAAGGACTGTCGAACGCCTGAACGATATGTTAGGC 495	Db 257 GlyThrGlyGlyGlyGlyAsnAlaGlyAsnGlyGlyAsnGlyGlySerAlaGlyTrp 276	Qy 376 AGCATGATGGGCGGTGGTGGCTGATGGGCGGTGGCTTAGGCGGTGGCTTAGGTAATGGC 435	Db 239 ArgGlyGlyAspGlyGlySerAlaGlyTrpLeuSerGlyAsnGlyGlyAspAla 256	QY 316 AATCAAAATGATACCGTCAATCAGCTGGCTGGCTTACTGACGGGCATGATGATGATGATG 375	Db 223 GlyAsnGlyGlyAlaGlyGlyAlaGlyGlyAlaGlyGlyAlaGlyGlyAlaGlyGly 238	Qy 256 GGTACCAGTCGCCAGAATGCTGGGTTGGGTTGGGTAATTCTGCACTGGGCGGGTGGGCGGCGGT 315	DD 203 IIEGIYAIGE196IYYAIAIGGIYAIGGIYGIYAIGGIYGIYIIIIAIGGIYDEGENE 222	130 (130)		YA68 MYCTU (1-463)	1 Gaps:	Best Local Similarity: 31.85% Mismatches: 112	248.00 Matches:	Length:	SQ SEQUENCE 463 AM; 39300 MW; CES090A/E9093902 CMC04)	2).
SEQ12-SEQ4 (1-1390) x Y034_MYCT	DB: 9.798	Score: 248.00	ment Scores:	5		-	Pfam; PF00934; PE; 1	DR TubercuList; Rv2634c; DR InterPro; IPR000084; PE_re	TIGR	Z80225; CAB		CC entities requires a licens		betw	This	CC SUBFAMILY. BELONGS TO	Submitted (APR-2001) to			Kolonay			RL Nature 393:537-544(1998).	"Deciphering		Hornsby T., Jagels K. Oliver S., Osborne J.		RA Cole S.T., Brosch R., Park RA Gordon S.V., Eighmeier K.,	RX MEDLINE-98295987; PubMed=9		OX NCBI_TaxID=1773;	OC Bacteria; Actinobacteria; OC Actinomycetales; Corynebac		DE Hypothetical PE-PGRS family			ž	RESULT 7

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Parkhill J., Carnier T., Churcher C., Harris D.,
Fx., Gas S., Barry C.E. III. Tekala F.,
Brown D., Chilloworth T., Comor R. Froy
Brown T. Good Care Sandas S. Murry B. J.
Quell M.A. Belandram M.A. Boges J.,
Selton S., Squares S., Squares R.,
C., Whitehead S., Brotll B.G.;
C., Whitehead S., Brotll B.G.;
C., Whitehead S., Brotll B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             st sequence update)
st annotation update)
illy protein Rv2634c.
Y441.04C.
                                                                                                                              D. Eisen JA., Carpenter L., White O.,
Joson R., Gwinn M.L., Haft D., Hickey E.,
Junayam L.A., Ermolaeva M.D., Salzberg S.L.,
Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinobacteria (class); Actinobacteridae; cterineae; Mycobacteriaceae; Mycobacterium.
he EMBL/GenBank/DDBJ databases.
O THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                  of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .778 AA
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TU (1-778)

88	660	
88	1044	
8888	984	964 GETATICGGTATGAAAAGCGGG
588	620	ValdiyGlyThrGlyGlyMetGlyGlySerGlyGlyValGlyGlyAsmGlyGlyAlaAla
333	963	
RA S	951	CTGCAAAACCTGAGCGGGCCGGTGGACTACCAGCAGTTAGGTAAC
R R R R	906	871 ACGGTTTTACCGTTCOTCG
2222	870	### ##################################
2223	541	GlyAlaLeuGlyAlaAlaGlyGlyAsnGlyGlyThrGlyGlyAlaGlyGlyAsnGlyGly
202	10	
222	798	766 TATAAAAAAAGGATCACTGATGGGCTGTGGGGC
P R R	501	 GlyAlaThrGlyGlyValAspGlyGlyValGlyGlyAlaGlyGlyGlyGlyGlnGly
RN	765	GGCACCCAGGGCAGTTCCTCTGGGGGCAAGCAGCCGAACGAA
888	708 481	649 CAGCAGCTGCTGAAGATGTTCAGCGAGGTAATGCAAAGCCTGTTTGGTGATGGGCAAGAT
2222	473	by TOCKARACKACKTICKCTCUGGRAKATTOCACTICAGATICAGGRACKGACKGATG :::
	463	alaGlyGlyThralaGlyThraspGlyGlyAlaGlyGlyAlaGlyGlyAlaGlyGlyIle
10 TE	588	AACAATAGCACTTCAACAACAACTTCCCCGGCTGGACCAGGGGCTGGGTATTAACTCAACG
B B 4	528	469 TCGAAACGCCTGAACGATATGTTAGGCGCTTCGCTGAACACGCTGGGCTCGAAACGCGCGCTCGAAACGCCCTCGAAACGAACG
2 8 5	432	415 GECOGTOCCTTAGGTANTGCTTGGGTGGGTGGGGTGGCGGAAGGACTG
2 B 1	414	355 ACCGGCATGATGATGATGATGATGATGAGCGTGTGAGCGCTGATGGGCGGTTAA 405GlyGlyAsnGlyGlyEroGlyPro
2 8 5	354	307 GGCGGC
2 B 1	392	247 GGGTTGCTGGCTACCAGTTGGCCAGAATCTCGGTTGGGTTGGGTTGGAATCTGCACTTGGGCTG
OV B	372	193 GGCTGGGAGCGTCAACGATGCCAAATTTCTATCGCCGGTGCGGCGGAAATAAC 193 GGCTGGGAGCCTCAACGATGCCAAATTTCTATCGCCGGTGCGGGC
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Wed Jan 15 11:31:40 2003 seq12-	seq12-seq4.n2p.rsp
DR EMBL; AL021930; CAA17353.1; DR EMBL; AL005936; AA444511.1; ALT_INIT. DR TIGR; MT0231;	Oy 814 CTGAGCCAGCTCCTTGGCAACGGGGGACTGGGAGGT Db 578
InterPro: IPR000084; PE_regio	850
SIGNAL 1 30 CHAIN 31 957	QY 877 CTTGACGGTTCCTCGCTGGCGAAAGGCTACAAAACCTGAGCGGGCGG
CONFLICT 40 40 CONFLICT 158 163	Db 613GlyfleAlaThrGlyAlaGlyGlyFleGlyGlyAlaGlyGlyAlaGlyGlyVal
CONFLICT 807 807 R -> G (IN REI SEQUENCE 957 AA; 81905 MW; 71EBABD417FF	QY 937 CAGCAGTANGGTANCGCCGGGGCACCGGT ACCGCTAGCAGT Db 631 SerLouLaulleGlySerGlyGlyThrGlyGlyAsnGtyGlyAsnSerIleGlyVal
4.11e-08 241.50 35.10%	Oy 979 GCGGGCATTCAGGGGCTGAATGAFATCGGTACGCACAGGCACAGTTCAACCCGTTCTTTC Db 650 AlaGlyLlaGlyGlyAlaGlyGlyArgGly
ty: 25.83% Mismatches: 9.54% Indels: Gaps:	1039 GTCAATA
SEQ12-SEQ4 (1-1390) x Y278_MYCTU (1-957)	OV 1099 GAGGTGTTTGGCAAGCCGCACTACCAGAAAGGCCCGGGTCAGGAGGTGAAAACCGATGAC 1158
Oy 178 AGTCTGAATACAAGTGGGCTGGGAGCGTCAACGATGCAAATTTCTATCGGCGGTGCGGGC 237 Db 362 ThickattiralaGlyGly11GdlyGlyAla	665
Oy 238 GGAAATAACGGGTTGCGTGGGTACCAGTCGCGCAGAATGCTGGGTTGGGTTGGGTGGC 288 IIIIII IIIIIII IIIIII IIIIII IIIIIII IIIIII IIIIII IIIIII IIIIII IIIIII IIIIII IIIIIII IIIIIII IIIIIII IIIIIII IIIIIII IIIIIIII IIIIIIII IIIIIIII IIIIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	b 673
289aattetigegeetigegegegegegataateaaaatgatacegteaateaget	Oy 1219 GAGCAGTTCARCAAGCCAAGGCATGATCAAAAGGCCAGCGGGTGATAACCGCAAGC 2218 Db 674HisGlyAlaAlaGlyGlyValProAlaGlyValGlyAlaGlyGlyAsn 690
OV 346 GGCTTACTCACCGGCATGATGATGATGATGAGCATGAGGGGGGGG	OY 1279 GGCAAGCCACGCGTGCCGGTGTTCTTCGCTGGGTATTGATGCCATGATGGCC 1338
408 GlyThrvalPheGlySerGlyGlyAlaGlyGly	691 GlyGlyLeupheAlaAsmGlyGlyAlaGlyGlyAlaGlyGlyPhe
Oy 406GOTGGCTTAGGCGTGGCTTAGGTAGGTAGGTGGCTGAGGTGGCCTG 456 ::	bb 710 GłykańciyciykanciyciyteubheGłyfhrciygiy 722
457	98
OV 484 GATATGTTAGGCGGTTCGCTGAACACGCTGGGCTCGAAAGGCGGGAACAATACCACTTCA 543	
459 GlyGlyIleGlyGlyThrGlyValLeuIleGlyAsnGlyGlyAsnGlyGlySerGly	
ACAACAAATTCCCCGCTGGACCAGGCGCTGGGTATTAACTCAACGTCCCAAAACGAGGAT	Mycobacterium tuberculosis. Mycobacterium tuberculosis. Bacteria; Actinobacteria; Actinobac
478 GlyTleGlyAlaGlyLySAlaGlyValGlyGlyValSezGlyLeuLeuLeuCeuGlyLeuAsp	
bb 498 GlyPheAsnAlaProAlaSerThrSerProLeuHisThrLeuGlnGlnAsnValLeuAsn 517	
Qy 664 ATGTTCAGCGAGATAATGCAAAGCCTGTTTGGTGATGGGCAAGAT 708	
ProPheGlnThrLeuThrGlyArgProLeuIle	
Qy 709 GGCACCCAGGGCAGTTCCTCTGGGGGCAAGCAGCCGACCGACCGAAGGCGAG 756	RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., RA Oliver S., Osborne J., Quali M.A., Rajanteam M.A., Rogers J., RA Ritter S. Seaner W. Kyelton S. Somarres S. Somarres R.
757 CAGAACGOCTATAAAAAGGAGTCACTGATGCGCTGTCGGGCCTGATGGGTAATGGT	
nh 558 AsnGlyThrProGlyThrGlyAlaAlaGlyGlyAlaGlyGlyTrnLauphoGlyAsnGly 577	

Wed Jan 15 11:31:40 2003

	÷	SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS SUBFAMILY.
	This betwee the H use modil entit	MRIS-PRO GRTY, is copyright, it is profused through, a collaboration man the Swiss institute of Bodicomatics and the BMG contration of Auropean Bodicomatics in the BMG contration on the by one profit institutions as long as its content is in on way the service of the BMG contration of o
919 9 2 2 2 2 2 2 2 1	EMBL: Tube: Inter Prope Prope Hypot SIGN/ CHAIR	BMIL, AUG2022, CAA1745.1. Theorotist review Freedom Fr
	SEQUENC	NCE 1901 AA; 147627 MW; C7B1923D5D0146CD CRC64;
red. core: prcen est t	red. No.: core: core: srcent si srt Local sery Matc	Lignment Secres: 5.18e-08 Longth: 1901 red. No.: 440.00 Secretary 21 rooms Eunitarity: 29.88 Longth: 180 sec. Longth: 18181arity: 29.88 Lindsatus: 1818 sec. Longth: 29.88 Lindsatus: 29.88 Lindsatus: 1818 sec. Longth: 29.88 Lindsatus: 2
, 612	199 1133	((1-1390) x Y208_MYCTU (1-1901) GGAGGTCAMCGATGCAMATTACGATTCCTATCCGCGGTCCGGGCCGAMATTACGGGTTGCTG 255
0 ~	256 1153	GTACCAGTCGCCAGAATGCTTGGGTTGGGTGGCAATTCTGCACTGGGGCTGGGC309
~	309	309
U	1169	GlyGlyThrGlyGlyAspGlyGlyAspAlaGlySerGlyGlyGlyGlyGlyPheGlyGly 1188
0 ~	310 1189	
0 ~	340 1209	CTGGCTGGCTTACTCACCGGCATGATGATGATGATGAGCATGATGGGCGGTGGTGGGCTG 399 AlaSrciyJeuGlyLeuGlyLeuGserGlyPheAspGlyGjyGlnGlyGlyGlnGlyGly 1228
0 ~	400 1229	ATGGGCGGTGGCTTAGGCGTTAGGTAATGGCTTGGGTGGCTCAGGTGGCCTG 456
0 ~	457 1249	GGCGAMGGACTGTCGAMCGCGCTGAMCGATATGTTAGGCGGT 498 GLYALaGLYGLYALAGFCANLAThfrain::::::
0 ~	499 1269	TCGCTGAMCMCGCTGGGCTCGAAGGCGGCAMCMATACCACTTCAMCAMCAMATTCCCCG 558 GlyGlnGlyGlyTiestyGlyAspGlyGlyAsn-AlaGlyPhGlyGlaGlyValfcoG 1288
-	559 1288	CTGANCAGGCGTTGGTATTBACTCAACGTCCCAAAACGACGATTCC 606 1yAspG1yG1yAspG1yG1yAsnA1aG1yPh6G1yA1aG1yPa1PTC-G1yAspG1yG1y 1307
_	607	GCGACCCGATGCAGCAGCTGCTGAAGATG 666
`	6	TCAGCGAGATAATGCAAAGCCTGTTTGGTGATGGGGAA

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SEGMENCE PROM N.A.
STRALMENTZWE PROM N.A.
STRALMENTZWE PARCHASTON, PARCHAST T., Churcher C., Barris D.,
Gozdon S.V., Elghaeler K., Gas S., Barry C.E. III., Peals F.,
Baccon S.V., Elghaeler K., Gas S., Barry C.E. III., Peals R.,
Baccon K., Dashan D. Broon D. Chillingerth T., Comnor E.,
Baccon K., Dashan K., Pethal T., Gondon J., Mariat R., Molreyd S.,
Bornady T., Sepals K., Kreyh A. T., Mariat S., Marphy L.,

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TCTGGGGGCAAGCAGCCGACCGAAGGCGA	727	Ş.
0	1130	8
10 AGCGAGATANTGCAAAGCCTGTTTGGTGATGGGCAAGATGGCACCCAGGGCAGTTCC 726	670	ę

A;Gene: Rv2490c C;Superfamily: collagen alpha 1(IV) chain

Page 3

	76	Qy 99	Db 34	0у 94	N) 6	D	Db 90) h	77	Db 28	Qy 7.1	Db 27		Qy 59	24	Q y 53	22	Qy 47	20	Qy 43	18	37	pb 17	Qy 31	16	ΩУ 25	Oy 19	SEQ12-SEQ4	Alignment. Pred. No.: Score: Score: Percent Si Best Local Query Matc DB:
erloritered ariumosicalogical or usus alumentarial trans arium busca e	vClvalaGlv-GlvAlaGlvG	GTACGCACAGGCACAGTTCAACCCGTTCTTTCGTCAATAAAGGCGATC	1 AlaAlaGlyGlyAspGlyGlyAlaGlyGlyAsnGlyGlyAlaGlyGlyAsnGlyGlyVal 360	0 CAGTTAGGTAACGCCGTGGGTACCGGTATCGGTATGAAAGCGGGCGATTCAGGCGCGTG 996	AladlyGlyAlaGlyGlyAlaGlyAlaThrGlyIleAsnGlyProAlaGlyIleSer 34	E.B. DYCOVALOYDDADDADDADDADADAYAYAYAYAYAYAYAYAYAYAYA	Cliustancossancioson Selections Cliustance Communication Cliustance Communication Cliustance Cliustance		AAAGGAGTCACTGATGCGCTGCGGGCCTGATGGGTAATGGTCTGAGCCAGCTC BZ	1 SerhspGlyGlyAspGlyGlyAla		5	ProGlyGlnAspGlyAlaAlaGlyValAlaGlySerAspAspGlyAlaGly 2:	CCACCTCAGACTCCAGCGACCCGATGCAG 6	4 GlyValGlyGlyVal	CAGGCGCTGGGTATTAACTCAACGTC	GlyAla-tGlyGlyAsnAlaGlyTrpPheGlyHisGlyGlyAlaGly 243	S.	9 AlaGlyLeuPheGlyAsaGlyGlyAlaGlyGlyAlaGlyGlyAlaGly 228	3	GlyGlyGlyValGlyGlyMetGlyGlyAlaGlyGlyAlaGlyGlyAlaGlyGlyAsa 20	GCATGATGGGGGGGGTGGTGGGCT	8 GlyThrGlyGlyThrGlyGlyTrpLeuAlaGly	8	2 PheGlyIleGlyGlyAlaGlyGlyAlaGlyGlyAlaGlyAlaProGly 177	3 CTGGGTACCAGTCGCCAGANTGCTGGGTTGGGTGGCAATTCTGCACTGGGGCTGGGCGGC 312	363 GGGCTGGGAGCCTCAACGATGCCAAATTTCTATCGGCGGTGCGGGGGGAAATTACCGGGTTC 32 	24 (1-1390) x A70869 (1-1660)	Manut. Seorces: 1.26e-11 Length: 1660 1.26e-12 Annual Length: 129 1.26e-13 Annual Length: 129

11/4 GOATTGAGCAAGGAAYGAACGACGGAAYGAACGACGAGAYGAACGACGAGAYGAACGACAGAA 1233	Db UY	Oy 250
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USANGGAMATCUTCATTCATTCATTGACCAGTATTCGCGCAAGCCGCAAGCAGTAC		Oy 133 GTGGGGGGGTAGGTFGGAATHTTCATAAGAGGAFAGGTFAGGAGTGGATACAAGT 192 Db 343 ValOlyAlaTieGinTieAseValTyrGlyGlyGerTieGluThtrasp 358
658 ValGLy		SEQ12-SEQ4 (1-1390) x E95965 (1-2174)
1003 ATCGGTACGCACAGGCACAGTTCAACCCGTTCTTTCGTCAATAAAGGCGATCGGGGGATG 1062		10.17% Indels: 2 Gaps:
952 GCCGTGGGTACCGGTATCGGTATGAAAGCGGCATTGCAGCGCCGTATGATGAT 1002 952 GCCGTGGGTACCGGT	Db Qy	Pred. No.: 1.7e-11
892 CTGGGCGCAAAGGCCTGCAAAACCTGAACCAGCCAGCCGATGAACTAACCAGCAACGTAACGACCAGCAACGCAGCAGCAGCAGCAGCAGCAGCAGCA	B 04	Alignment Scores:
:::	Db	A:Contents annotation G:Genetics:
GGTANTGCTGGCACGGGTCTTGACGGTTCGTCG	Qy	neogult, P.: Vandenbol, M.; Vorholter, F.J.; Weldner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Title: The composite genome of the legume Thiont Snorhizobium meliloti. A:Deference number, 160304, WITE-2130324, https://doi.org/10.1003/
817 AGCCAGCTCCTTGGCAACGGGGGACTGGGAGGTGGTCAG	Db 07	L.: Hyman, R.W.; Jones, T. Science, 293, 668-672, 2001 Science, 293, 668-672, 2001 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A:Authors: Kahn, M.L.; Kalman, M
	Db 5	A:EXperimental source: strain 1021, megaplasmid pSymB A:EXperimental source: strain 1021, megaplasmid pSymB R:Gallbert, F.; Finan, F.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreamo, S.; Federspiel, N.A.; Fisher, R.F.;
544 ileLeuSerIleGlyGlyThrGlyGlyAsnAlaAsnTyrAlaGlyAsnAlaGluvalGln 563 769 AAAAAAGAGGAGTGAGT	OV Db	A:Molecule type: DNA A:Molecule type: DNA A:Residues: 1=2174 <kub> A:Crows=references: GB:AL591985; PIDN:CAC49389.1; PID:q15140875; GSPDB:GN00167 A:Crows=references: GB:AL591985; PIDN:CAC49389.1; PID:q15140875; GSPDB:GN00167</kub>
721AGTTCCTCTGGGGGCAAGCAGCCGACCGAAGGCAGAACGCCTAT 768	Qy	A; Accession: E95965 A; Status: preliminary
90/ III.AMACAMARIATUCAANACCENTITT" - GATUATUGGGAGAMATIGGGAGAGATGGGACAGAGGC /20 90/ III.AMACAMARIATUCAANACCENTITT	B 5	Proc. Natl. Acad. Sci. U.S.A. 96, 989-9999, "Communication of Communication of Communicatio
SerAlaGlyAlaAlaSerValGlnAsnThrGlyAlaIleThrThrAspGlyTyrSerAla	Db Db	C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C:Accession: E99965
607 ACCTCCGGCACAGATTCCACCTCAGACTGCAGCGACCCGATGCAGCAGCTGCTGAAGATG 666	Qy	hypothetical glycine-rich protein (imported) - Sinorhizobium meliloti (strain 1021) maga C; Species: Sinorhizobium meliloti
IlealaGluGlyLeuThrLeuGluLeuGlyGlyAspGlyGlyGluGlyGly	Db .	RESULT 4
467 GlyGlyHlaSerTyr6lyIleLeuvalGlnSerTleGlyGlySerGlyGlyThrGlyGly 486 547 ACAAATTCCCCGCTGGATCAGGCCTGGGTATTAACTCAACGTCCCAAAACGACGATTACC	OV D	Db 435 GlyshadglyshastgalaglyAlaksnGlytenhlanlaglyssnspgly 451
	οy	417
452 AsnThrAlaThrIleAsnAsnAlaGlyGlyThrIleSerThrSer 466	Db	Qy 1258 ATGGCGGGTGATACCGGGAAACCTGCAGGCACGGGGTGCCGGTGGTTCTTCGCTG 1317
CTGAACGATATGTTA	Qy	Db 416GlyH 417
	Db	1198 GGAATGACACCAGCCAGTATGGAGCAGTTCAACAAAGCCAAGGGCATGATCAAAAGGCCC
OCTOSCTTAGCCGCTGGCTTAGCTAATGGCTGGCTCAGCTCA	Qy	411
	Db .5	1138 CAGGAGGTGAAAACCGATGACAAATCATGGGCAAAAGCACTGAGCAAGCCAGATG
398GlyValGlyAlaTyrValThrThrGlySerLys1leThrThrThrGlyAspPheSer 416 346 GGCTTACTCACCGGCAVGATGATGATGATGATGAGTGGGCGGTGGTGGTGATGGGC 405	Q D	The control telephoconstatic consocial telephocococy and the consocial telephocococy and telephocococy and telephococococy and telephococococococy and telepho
	9	380
379 AspAspThrAlaValValGlyThrSerGlyGlyGlyGlyPheGlyGlyAsnAlaGly 397	рb	1057

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ANGENCICANCICANCICANCICA (ANGELIA CONTROLLA CO	640 GACCCGATGCAGCAGCAGCACAAACACTCCCAAAACCCCGATTTCGCTCAT 699 10 626

seq12-seq4.n2p.rpr

SEQ12-SEQ4	Db 343 ThrGlyGlyAsnGlyGlyvelGlyAlaProGlyGlyAlaGlyGlyAsnGlyGly 360
DB:	QY 817 AGCCAGCTCCTTGGCAACGGGGGACTGGGA846
Best Local	Db 330GlyAlaThrGlySerSerAlaSerGlyGlyAsnGlyAla 342
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Alignment S	Db 313 AspGlyAlaProGlyGlyAsnGlyGlyAsnGlyGlySerValGluHisThr 329
C;Superfami	OY 697 GATGGGCAAGATGGCACCCAGGGCAGTTCCTCTGGGGGCCAAGCAGCCGGACGGA
C;Genetics:	Db 308 G1yG1yAlaG1yG1y 312
A: Experimen	Oy 637 AGCGACCCGATGCAGCAGCTGCTGAAGATGTTCAGCGAGATAATGCAAAGCCTGTTTGGT 696
A; Molecule	Db 288 GlyAsnAlaSerThrSerGlyGlyIleGlyIleAlaGlnThrGlyGlyAlaGlyGlyAla 307
A; Accession	Oy 592 CANANGGACGATTCCACCTCCGGCACAGATTCCACCTCAGACTCC 636
A;Title: De	Db 268 GlyAlaAspGlyAlaAsnGlySerAlaIleGlyGlnAlaGlyGlyAlaGlyGlyAspGly 287
Nature 393,	Oy 532 ANTACCACTTCAACAACTTCCCCGCTGGACCAGGCGCTGGGTATTAACTCAACGTCC 591
9.5	Db 248 ProAlaAlaAsnGlySlyAsnGlyLeuAsnLeuValGlyValProSlyThrAlaGlyGly 267
C,Accession R,Cole, S.T	ACG
C:Species:	Db 228 GlyGlyAlaGlyAlaAlaGlyVelAsnAleVelAsnProGlyLeuAlaThrProVelThr 247
H70846	QY 448 GGTGGCCTGGGCGAAGGACTGTCGAACGCTGAACGATATGTTA492
SULT 7	Db 208 GlyAlaGlyGlyAspGlyGlyAsnAlaGlyPhePheGlyAsnGlyGlyAsnGlyGlyMet 227
Db 499 G	Oy 418 GSTGGCTTAGSTAAT
1327	Db 188 PheGlyGlyAsnGlyGlyAlaGlyGlyIleGlyValAlaGlyIleAsnGlyGlyLeuGly 207
481	QY 373 ATGAGGATGATGGGCGGTGGTGGGGCTGATGGGC
Оу 1267 G	Db 177 GlyAlaGlyGlyThrAlaGlyTrpPheFheGly 187
Db 468 -	
Oy 1219 G	
Db 454 A	CTGGGTACCAGTCGCCAGAATGCTGGGTTGGGTTGGGTGGCAATTCTGCACTGGGGCTGGGCGGC
Qy 1159 A	
Db 450 -	193 GGGCTGGGAGCGTCAACGATGCAAATTTCTATCGGCGGTGCGGGCGG
0у 1099 сы	SEQ12-SEQ4 (1-1390) x B70523 (1-591)
Db 437 I	2 Gaps:
Oy 1039 G	10.07% Indels:
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preliminary; nucleic acid sequence not shown; translation not shown e type: DMA e e ty

imilarity: 1 Similarity: ch: nily: collagen alpha 1(IV) chain Scores: 2.51e-11 255.00 36.14% 29.49% 10.07% Length: Matches: Conservative: Mismatches: Indels: Gaps: 1538 133 30 167 122 23

(1-1390) x H70846 (1-1538)

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551	ClyGlyAlaGlyGlyValSerAlaasnProAlaLeuAsnGly	538
	CANTAMOGICGA TUGGGCAT	51 03
17	laGlyAspGlyGlyAlaGlyAlaAlaGlyAspValThrLeuAla	5
1038	ATTCAGGCGCTGAATGATATCGGTACGCACAGGCACAGTTCAACCCGTTCTTTC	979
978 502	DEGTGGACTACCAGCTAGGTAACGCCGTGGGTACCGGTATGGAA 	919 490
918 489	GENANTICTGGCACGGGTTTTGAGGGTTGGTGGTGGGGGGGGAGGGGGGGAGGGCTGAAAGCTG	859 470
858 469	CAGGGC SerGly	814 451
813 450	CGCTGTCGGGCCTGATGGGTAATGGT 1yHisGlyGlyAsnGlyGlyAsnGly	754 434
753 433	GAAGGC GlyGly	414
413		412
693	30GACCOGATGCAGCAGCTGCTGAAGATGTTCAGCGAGATAATGCAAAGCCTGTTT	634
633	GGTNTTANCTCAAGGTCCCAAAACGAGGRTTCCACCTCCGGCACAGATTCCACCTCAGACGLTATAGAAGAACGAAGACTAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	574 393
573 392	GGCGCTG nAlaGly	514 374
513 373	CTGGGCGAAGGACGCCGAACGGTATGTTAGGGGTTGGCTGAAAGGTG CTGGGCGAAGGACGCTGAACGATATGTTAGGGGTTGGCTGAAAGGTG AlaGlyGlyLeuLeuAlaGlyAlaHisGlyAlaAlaGlyAlaThrProThrSerGly	355
453 354	GETGGCTTAGGCGCTTAGGTATAGCTTGGGTGGCTDAGGTGGCTAAGGTAGTGGCTTAGGTAGTGGTTAGGTAGTGGTTAGGTAGTGGTAGTGGTAGTGGTAGTGGTAGTGGTAGTA	406 335
334	/GlyAlaGlyAspProSerPheAlaValAsn	315
314	yLeuLeuValGlyasnGlyGlyAlaGlyGlyAla	99
393	GCATGATGATGATGAGCATGATGGGGGGTGGT	337
336 298	GOACTGGGGGGGGGGGTAATCAAAATGATRACGGTGAAT 	295 279
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252 262	AATTTCTATCGGCGGTGCGGGCGGAAATAACGGGTTG 	193 249

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1137 TCAGGAGGTGAAAACCGATGACAANTCATGGGCAAAAGCCACTGAGCAAGCCAGATGACGA 1196

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OY 1211 GCTGGTGTATTCGTCGTCATCTGGCTTGCTCAGGCTTTTGCCATGATTTGTCATCG 1152 Db 251	Oy 1271 GYATCACCCCCCATGGCCTTTGATCATGCCCTTGGCTTTGGTTTGACTCCCCCATACTG 1212 Db 239 rSarSarFocPorPocAlaSThArysarPopTo250	Oy 1319 CCCAGCAGGAGACCACGGGCACCGGTGG	Oy 1379 GCGCCOACTTGCCANGTGCCATATTGTTANTGGCATCACCGGCCATCATGGCATCATGCATCATATA 1320 III III III III III III III III III I	9.78% Indels: 2 Gaps:	2 78e-11 Langth: 66 Prod 30:	A/Cross=references: BML:X65165, NID:g21991; PIDN:CAA46283.1; PID:g21992 C;Reywords: glycoprotein Altomate Gorge.		matrix	828699 Volvox carteri (fragment) C.Species: Volvox carteri (fragment) C.Species: Volvox carteri (fragment) C.Species: Volvox carteri (fragment)	dy 139 GOODGOOGGOOGGOOGGOOGGOOGGOOGGOOGGOOGGOO	964	LaAlaGlyAsnG			9001	Db 900 GIYASHGIY	AG (5)	Qy 931GACTACCAGCAGTTAGGTAACGCCGTGGGTATCGGTATCGGTATG 975
RESULT 11 P70971 c. 11 Probletical glycine-rich protein Bv387 - Mycobacterium tuberculosis (Strain M37RV) C.Species: Mycobacterium tuberculosis	Oy 209 GYTGAGGCTGCCGAGCCA 192 Db 434 AsgNaphlaPropropro 439	Oy 260 GTACCCAGCAGCCAGTATTT	320 TGATTACCGCCGCCCAGCCCCAGTGCAGA.	Oy 380 ATGCTCATCATCATCATGCGGGTAGTAGGCGAGCTGGTTGAGGGTATCATTT 321 Db 397	Oy 440 CCAMACCATHOCHMICACCCCAMACCANCCANCANCANCANCANCANCANCANCANCANCANC	Oy 494 CCTMACATRICGITCAGCGCGTCGCCCAGCCCAGCCCCAGCCCAA41 Db 368 Pro Propropropropropropropropropropropropropr	Oy 554 GARTTOTOTOTOGAGGGATATOTOGGGGGGGGGGGGGGGG	0y 614 CCGGAGGTGGAANCGCGGTTTTTTTTTTTTTTTTTTTTTT	Oy 674 TCGCTGAACATCTTCAGCAGCTGCATCGGGTGCGCTGGAACTCTAGGGGAACTCTAGGGGAACTCTAGGGGAACATCTGAGGGAACATCTGAGGGAACATCTGAGGGAACATCTGAGGGAACATCTGAGGGAACATCTGAGGAACATCTGAGGAACATCTGAGGAACATCTGAGGAACATCTGAGGAACATCTGAGGAACATCTGAGGAACATCTGAGAACATCTGAGGAACATCTGAGAACATCTGAGGAACATCTGAGGAACATCTGAGGAACATCTGAACATCTGAACATCTGAGAACATCTGAACATC	Oy 734 COCCEMANGEANCHGCCCTGGGTGCCATCTGCCCATCCCAAACAGGCTTTGCATTATC 675 Db 337 POTTOPTOSaffror Proprocyspositifi 337 POTTOPTOSaffror 348	Oy 794 GACAGCGCATCAGTGACTCCTTTTTTATAGAGGGTTCTGCTCGCCTTCGGCTCGGCTGGTTGG 735 Db 336	317	Gy 911 T6CASCCCTTTGCCGCCAGGAGAGAGCG TCAGAGCCGTGCCAGCATTACCGCC 835 Db 297 ValSerProSerProProProProAlaProValSerSerProProProProProProPro 316	Qy 971 CCGATACCGACGGCGTTACCTAACTGCTGGTAGTCCACCGGCCCCCTCACTTT 912 LI 1-11 1-1	Oy 1031 CGGGTTGAACTGTGCCTGTGCGTAACCGATATCATCCAGCGCTTTCAATA 972 Db 285	193 TOPICONTOANCESACCANTENCETICOCCOCCOCCOCCOCCOCTOCTENTIATICACCAAAGAA 193		Oy 1151 GTTTTCACCTCCTGACCCGGGCCTTTCTGGTACTGCGGCTTGCCAAACACCTCAGGATAC 1092

		11.5 17.1	RESULT F70971	
	AspAspAlaProProPro 439	434	Db	
	GTTGACGCTCCCAGCCCA 192	209	Qy	
433	roProLeuGlyThrArgProProProProProProGlu	417	DЬ	
210	GTACCCAGCAACCGTTATTTCCGCCCGCACCGCCGATAGAAATTTGCATC	260	Qy.	
416		399	DЬ	
261	a	320	Qy	
398	Serpro	397	Db	
321	GCCAGCTGATTGACGGTATCATTT	380	Oy	
396	ProAlaSerSerProProProProProProProProProProProProPro	379	DЬ	
381		440	Qy	
378	Pro	368	Db	
441		494	8	
367	ProproProproProproValValSerpropro	359	DЬ	
495		554	9	
358	ProProProArgSerSer	351	Db	
555	TGGGACGTTGAGTTAATACCCAGCGCCTGGTCCAGCGGG	614	9	
350	SerPro	349	Оb	
615	TGTG	674	Q	
348	ProProProSerProProProProArgProSerPro	337	Db	
675	ATC	734	Qy	
336		336	Db	
735	GACAGCGCATCAGTGACTCCTTTTTTATAGGCGTTCTGCTCGCCTTCGGTCGG	794	Qy	
336	ArgProSerProSerProProProProArgSerSerProSerProProProProSerPro	317	Db	
795		854	γQ	
316	ValSerProSerProProProProClnProValSerSerProProProProProProProProPro	297	Db	
855	-TCANGACCCGTGCCAGCATTACCGCCC	911	νο	
296		289	DЬ	
912	CCGATACCGGTACCCACGGCGTTACCTAACTGCTGGTAGTCCACCGGCCCGCTCAGGTTT	971	γQ	
288		285	Db	
972	GATATCATTCAGCGCCTGAATGCCCGCTTTCATA	1031	νo	
284	rProProProProArgValProProSerProProPro	271	Db	
1032		1091	Q	
271	glleThrSerProSerProValLeuThrAlaSerProProLeuProLysThrSe	253	Db	
1092		1151	Q	

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Qy 1214 CIGGCIGGIGACTICGGICATCGGCTTGGCTCAGTGCTTTTGCCCATGAT 1161	Db 445 GlyAsnGlyGlyAsnGlyGlyAsnGlyGlyThrGlyGlySerGlyGlyValGly 462
SEQ12-SEQ4 (1-1390) x E86255 (1-744)	CTGAGCCAGCTCCTTG
ty: 27.64% 9.78%	Oy 748 GAMGGGGGCAGAMGAGGGCTATAMAMAMGGGTCACTGATGGGCTGCTGCGGCCTGAETG 804 Db 425 GlyGlyArgGlyGlyAspGlyGlyScrGlyGlyAlaGlyGlyAlaGErGlyTrpLewWet 444
2.96e-11 Length: 253.50 Matches: milarity: 38.44% Conservative:	valdlydlyAspGlyGlyAspClyGlyAsnGlyGlyThrGlyGlyThr
Alignment Scores:	688 CTGTTTGGTGATGGGCAAGATGGCACCCAGGGCACTTCCTCTCTGGGGAAGGAGCGGCACC
A:Cross-references: GB:AE003172; NID:g3157926; PIDN:AAC17609.1; GSPDB:GN00141 C:GenetLcs: A:Map position: 1	Oy 628 TCMGACTCCAGCGACCAGCAGCAGCAGCAAGATGATTCAGCGAGATAATGCAAAAGC 687 Db 407
A:Status: preliminary A:Nolecule type: DNA A:Nolecule type: DNA A:Residues: 1-744 <sto></sto>	391 AlaGlyGlyValProAlaAsnGlnGlyGlyAsnSerAlaLeuGlyThr
A.Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A66141; MUID:21016719; PMID:11130712 A;Accession: E86255	Oy 568 GCGCTGGGTNTTAACTCAACGTCCCAAAACGACGATTCCACGTCGGGCAGAGTTCCACC 627
A.Authors Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A.Authors Salzberg, S.L.; Sriwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.	508 ACCCTGGGCTCGAAAGGCGGCAACAATACCACTTCAACAACAACTACCCCGCTGGACCAG
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia	
Chin, C.W.; Chung, H.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Credsy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000	DD 342 KLBULÝVLÝMITULÝTIEKSTULÝHISKLBULÝGLÝKLBULÝ"-"GLÝKLBULÝVLÝKLB JOU OY 448 GOTGGCOTGGGGGANGSACTGTCGANGGGGCTGANGGATNTGTTNGGCGGCTTTGGCTGANG 507
C;Accession: E86255 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon	400 ATGGGCGGTGGCTTAGGCGGTGGCTTAGGTAATGGCTTGGGTCGCTCA
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001	Db 322 AlaGlyGlyGlnAlaAlaSerAlaGlySerSerValGlyGlyAspGlyGlyAsnGlyGly 341
R86255	QY 340 CTGGCTGGCTTACTCACCGGCATGATGATGATGATGATGATGATGATGATGATGATGGGCTG 399
Db 574 GlyAspAlaPheAsn 578	303
Qy 1339 GGTGATGCCATTAAC 1353	280 TTGGGTGGCAATTCTGCACTGGGGCTGGGCGGGGGTAATCAAATGATACCGGTCAATCAG
bb 558 GlyAsnAlaAspSerThrAsnGlyGlyProGlySerAspGly	Qy 226 GGCGGTGCGGGGAANTAACGGGTTCCTGGGTACCAGTGCGCCAGAATGCTGGG 279
1070	SEQ12-SEQ4 (1-1390) x F70971 (1-588)
1219 GAGCAGTTCAACAAAGCCAAGGGCATGATC	10.01% Indels: 2 Gaps:
Oy 1159 AAATCATGGGCAAAAGCAATGAGGCAGATGACGAGGAGGGGGAAAGCAGCCAGC	2.87e-11 253.50 ty: 36.18%
	C:Superfamily: unassigned collagens Alignment Scores:
1099 GAGGTGTTTG	C:Genetics: A:Gene: Rv3367
Oy 1039 GTCANTAAAGGCANGGGAAGGGAANGGGTAAGTCANTGAGCAAGTANTCCT 1098	A;RESIQUES: L-588 <cul> A;CCOSS-references: GENALO09108; GB:AL123456; NID:g3242262; PIDN:CAA15752.1; PID:e120228 A;Experimental source: strain #37Rv</cul>
498	A; Notes and Figure 1997 A. A:Status: prediamary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA.
979	A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9834230
482	Nature 393, 537-544, 1998 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
OV 919 AGCGGGCCGGTGGACTACCAGCAGTTAGGTAACGCGGTGGGTACCGGTATCGGTATGAAA 978	RICCHE, S.II.; DIOSCHI, R.; PGLEMILL, J.; GMERINSE, T.; CHUICHER, C.; HBELLE, D.; GOTCON, B.; CONDOT, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Bajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
859	C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Feb-2000 C:Accession: F70971

The first fi	** TANCOGRACIO ACCOUNT ACT ANCIGOTA OF CANCERCIA CONTROL	1027 TTGAACTGTGCCTGCGGTACCGATATCATTCAGCGCCTGAATG	The control of the co	1267 107 1207 122	1387 81 1327 94	Alignment Scorces: 4.17e-11 Length: 358 Fred. Do. 2007 Scorces: Smilarity; 20.00 Conscious: 1.00 Conscious: 1.	tulion year) al. one-1988 teat_change C.J. 967 of a hydroxyproline-rich glycop (six4823; MID:3437892 WID:345348; PID:AAA33765.1; P MID:346548; PID:AAA33765.1; P de glycoprotean	TIGCATCGT
	924 867 vr 190		135 IGG 1028				21-Jul-2000 rotein gene family in ID:g169349	menc)

Qy 943 TTAGGTAACGCCGTGGGTACCGGTATGGGTATGAAAGCGGGC 984	Pred. No.: 6.47e-11 Length: 731
Db 658 GlyslyLysGlyCalGlyAlaAlaGlyClyLeuAlaGlyGin 672	Alignment Scores:
QY 904 GGG	A;Gene: Rv3388 C;Superfamily: elastin
Oy 847GRTGGTCAGGGCGGTATCCTGCGAGGGGTCTTGAGGGTCGTTGCTGCTGGGGGCAAA 903 Db 638 ValGlyAlathrGlyGlyAsmGlyGlySerGlyIlmGlyProAlaSerValGlyGlyAsm 657	A.Residues: 1-731 «COL» A.Rosidues: 1-731 «COL» A.Cross-references: GB:AL009198; GB:AL123456; NID:g3242262; EIDN:CNA15773.1; PID:g266166 A.Experimental source: strain H37Rv C.Genetics:
Oy 793 TCGGGCCTGATGGGTANTGGTANTGGTANTGACCAGCTCCTTGGCANCGGGGAC	A; Machaesian: C/0974; Mully:8629987; Mully:9638280 A; Accession: C/0974 A; Mattus: preliminary; nucleic acid sequence not shown: translation not shown A; Molacule type: DMA:
Db 603ValalaLeuSerValGlySerThrGlyGlyLeuGlyGlyAsnGly 617	A.Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
OV 745 ACCGAAGGCGAGCAGAACGCCTATAAAAAAGGAGTCACTGATGCGCTG792	Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamila, N.; Hotroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 193, 317-544, 1959
685 AGCCTGTTTGGTGATGGCCAGCACCCAGGCCAGTTCCTCTGGGGGCAAGCAGCCG	C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C:Accession: C7974
Oy 625 ACTIONANCICONGCONCOCNICONGCINGCINGCINGCINGCINGCINGCINGCONGCONGCINGCINGCINGCINGCINGCINGCINGCINGCINGCI	RESULT 14 C70974 Cal glycine-rich protein Rv3388 - Mycobacterium tuberculosis (strain H37RV) Kypothes: Mycobacterium tuberculosis C.Spotles: Mycobacterium tuberculosis
Oy 565 CHAGGGGGGGATATAACTCAAGGTCCAAAAAAAAAAACAATCCAACCTCCAGCAAAAATCCAACCTCCAACAAAAAAAA	Oy 180 TECHNA 180 Db 326 TyrLys 327
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532AATACCACITCAACAACAAATTTCCCCCGCTGGAC	245 TEATTTCCGCCGCACCGCCGATAGAAATTTGCATCGTTGACGCTCCCAGCCCACTTGTA
Qy 514 GGCTGGAAAGGCGGCAAC 531 III IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 305 ACCCCAGARATTECCACCCAACCCAGCATTCTGGGGACTGGTACCCAGCAACCCG 246
Oy 454 CTGGGCGAAGGACTGTGGAAGGCGCTGAAGGATGTTAGGCGTTGGGTGAAGAGGCTG 513 Oy AlaGlyGlyAsmThrAlaGlyArgArgAlaAspAlaileAlaGlyThr	OY 365 ATCATRICGGGTGAGTAGAGAGCTGATTGAGGTATTGATTTTGATTTTGATTTTGAGGCGCCC 106
Oy 18 667806778067	278
Oy 361 ATGATGATGATGACAMGAMGAGGGTGGGTGGGTAGGC	QY 4.32 U.A.***********************************
Oy 310 GGCGSTARCAMANGATACGTCAMTCACCTGCGTGGGTGACCTGGC 560 Db 456 GlyGlnLewTyrGlyAsnGlyGlyAspGlyGlyAsnGlyGlyGlyAsnGlyGlyAsnGlyGlyGlyAsnGlyGlyAsnGlyGlyAsnGlyGlyAsnGlyGlyAsnGlyGlyGlyAsnGlyGlyGlyAsnGlyGlyGlyAsnGlyGlyGlyAsnGlyGlyAsnGlyGlyAsnGlyGlyAsnGlyGlyAsnGlyGlyGlyAsnGlyGlyGlyAsnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	-
Oy 271	2/4 MANANCHANITAMANANTTYTTETTAMANISTATTGTTGCGGCTTTGCAGCCC
Db 416 GlyAsnalaGlyGeuileGlyAlaGlyGlyHisGlyGlyAlaGlyGlyAsn 435	233
402 SerAlaGlyThrGlyGlyValGlyAlaserGlyGlyThrGly	DD 233 Ser 2000 23
Qy 178 AGTOTGANTACANGTGGGCTGGGAGGGTGANGGATGGAAATTTCTATCGGGGGGTGGGGGG 237	692 AACAGGCTTTGCATTATCTCGCTGAACATCTTCAGCAGCTGCTGCATCGGGTCGCTGGAG
SEQ12-SEQ4 (1-1390) x C70974 (1-731)	Db 218 Pro
9.83% Indels: 2 Gaps:	Qy 752 CCTTCGGTCGGCTGCCTTGCCCCAAGAGGAACTGCCCTGGGTGCCATCTTGCCCATCACCA 693
Score: 249.00 Matches: 96 Percent Similarity: 35.63% Conservative: 23 Best Local Similarity: 28.74% Mismatches: 101	Qy 812 CCANTANCECATCAGGGCGACCAGCGACCAGCGACTCAGTGACTCCTTTTTTATAGGCCTTCTGCTCG 753 LI III III Db 211 PF0F0F0F0F0F0F0F0F0F0F0F0F0F0F0F0F0F0F0

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Search completed: January 14, 2003, 17:12:24 Job time: 41 secs



SUMMARIES

Copyright OM nucleic - protein search Run on: January 14. 11.16: SB012-SB04	Copyright (c) 1929 2 7003 Copyright (c) 1929 2 7003 Copyright (c) 1920
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Scoring table:

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searched: Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext 908470 seqs, 133250620 residues 7.0

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Pred. No. is the number of results predicted by chance to have score of the result being printed, score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Length	DB	ID	Description
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	standard;		
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07-DEC-1998 (first entry)

Erwinia amylovora hypersensitive response elicitor (HRE)

Hypersensitive response elicitor; HRE; insect resistance, biological control; transgenic plant.

Erwinia amylovora

03-SEP-1998 W09837752-A1

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                                                                     Erwinia amylovora
                                                                                             Hypersensitive response elicitor; HRE; growth; transgenic plant.
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                                                                Hypersensitive response elicitor; transgenic plant; seed; pathogen resistance; disease resistance; crop protection.
                                                                                                                                      Hypersensitive response elicitor protein (39 kDa).
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DY 09-MAR-1999 (first entry) XX		415 GGCGTGSCTTAGGTAATGGCTAGGCTGGCCTGGCCGAAGGACTGTCGAAC 4/4	9
AAW87639 ID AAW87639 standard; Protein; 403 AA. XX AC AAW87639;		ACCGGCATGATGATGAGGAGCATGATGGGGGGTGGTGGGCTGATGGGCGGTGGGCTTA ACCGGCATGATGATGATGAGGAGCATGATGGGCTGATGGGCGGTGGGCTTA ACCGGCATGATGATGATGATGAGGAGGATGGGCTGATGGGCGGTGGGCTTA ACCGGCATGATGATGATGATGAGGAGGATGATGGAGGATGATGAGGATGAT	B 94
Oy 13/5 GGCGGGGT 1383 Db 401 GlyAlaAla 403 RESULT 4		295 GEACTGGGGCTGGGGGCGCTARTCAAANTGATACCGTCAATCAGCTGGCTTAGTC 354 41 ALLGGGTGGGGGGGGGGGTAATCAAAATGATACCGTCAATCAGCTGGCTG	Oy Db
		GGGGGAAATAACGGGTTGCTGGGTACCAGTCGCCAGAATGCTGGGTTGGGTGGCAATTCT	Db 99
Qy 1255 CCOXTGGCGGGTGGXTMCCGGGAAGGGCAACGTGCAGGAAGGGGAGGGGGGGGGG		175 ATGASTCTGATACCAGTGGGCTGGGGAGGTCAACGATGCAAATTTCTATCGGCGGTGGG 234	Db Qy
OY 1195 GACGGARTGGACCACCACTREGGACAGTCTAACCAAGGCCATGATCAAAGCCATGATCAAAGCCATGATCAACAAGCCATGATCAACAAGCCATGATCAACAAGCCATGATCAACAAGCCATGATCAACAAGCCATGATCAACAAGCCATGATCAACAAGCCATGATCAACAAGCCATGATCAACAAGCCATGATCAACAAGCCATGATCAACACCATGATCAAGCCATGATCAACACCATGATCAAGCCAAGCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAG		Indels: Gaps:	DB:
Oy 1135 GGTCAGGAGTGAAAACCARTGACAANTRAGCAAANGACAACGAAATGAC 135 GGTCAGGAGTGAC 135 GGTCAGGAGTGAC 136 GGTCAGGAGGAGGAGGAGGAGGAGGACAAACCAATGACAACGAGGAGGACGACGACGACGACGACGACGACGACG		1.61e-161 2079.00 100.00%	Pred. Score: Percen
Oy 1075 GGTCAGTGATGGACGAGTATCGTGAGGTGTTGGGCAAGCGGAGTACCAGAAAGGCGG DD 1075 GGTCAGTGATGGACGAGTATCGTGAAGTGTTGGGAAGCGCGAGTACCAGAAAAGGCGG DD 1075 GGTCAGTGATGATGATGAGGAGGAGGAGAGAGAGAGGAGGAGGA		Sequence 403 AA;	SXS
Oy 1015 AGGACATTCAACCCGTTGTTGTCATAAAGGGATGGGGAGTGGGAAAAGCAATCCGATGGGAAAAGCAATCAGAAGAAAGA		but not tomato. However, it elicits a hypersensitive response in tomato. Thus, E. anylovoza can be applied to tomato seeds to lapart pathogen resistance without causing diseases in plants of the tenerical	8888
Oy 95 GTGGTRACGGTRTCGGTRTGGTATGANAGGGGGTGTGAGGGGGTGATGAGGAGGAGGAGGAGGAGGA	Db Db	Ambeblish By G. 9.7 Cheek dan dan komboods combeblish betat by betat voor Ambeblish By G. 9.7 Cheek dan dan komboods combeblish betat betat by the service of the service	38888
y 895 GGGGGCANAGGGCTGCANANCTGAGGGGGCGGTGAGCTACAGCAGTAAGGGC 	Qy Db	Whit makecule including an HRE polypeptide or protein are used. HRE polypeptide or protein are used. HRE polypeptide sequences from Envira Chrysothems, Erwinia amylovota, Pendomonas Statementum, Manihomonas, Pendomonas Statementum, Manihomonas,	88888
OY 835 GGGGACTGGAACGGCGTAATCCTGGCACGGCTTTTGACGGTTCTTCCTCTCTT DE 221 GlyGlyLeuGlyGlyGlyGlyGlyAnnAlaGlyThrGlyLeuMspGlySerSerLeu DB 221 GlyGlyLeuGlyGlyGlyGlyGlyAnnAlaGlyThrGlyLeuMspGlySerSerLeu	Db.	of reads. Tsolated HRE proteins can be applied to seeds as a means of imparting pathogan resistance to plants grown from the seeds. Alternatively, bacteria containing the ones encoding the HRE can be and institutely, bacteria containing the ones encoding the HRE can be and institutely.	38888
y 775 GGASTANCSARGCCGTETGGGGCCTGATGGGTANGGTCTGATGCAACCAGCTCCTTGGGCAAC b 201 GlyVelThrAspAlaLeuSerGlyLeuMetGlyAsnGtyLeuSerGlnLeuLouGlyAsn	Оу	THE 3 THE 39 NOW INVESTIGATION OF THE TRANSPORT OF THE STATE OF THE ST	38888
y 715 cacacharrocrytosasachachachachachachachachachachachachacha	Qy Db	Typessensitive temporate electron pulypepting to seems Disclosure; Page 18-20; SSSp; English (TER) property of	2 2 2 2 2
y 655 GYGCTGAACATGTTCAGCGAANTANTGCAAGCCTGTTTGGTGATGGGCAAGTGATGCAAC	Qy ab	R-PSDB, AAV36428. R-PSDB, AAV36428. R-PSDB, AAV36428. Reparking pathogen resistance to plents - by applying a huntry pathogen resistance to plents - by applying a	R T X R S
y 595 AACARCANTCACCTCCGGCACACATTCCACCTCAGACTCCAGCGACCACCACCACCACCACCACCACCACCACCACCA	No etc	Beer SY, QUID. Wel 2;	2222
Y 515 ACCACTTCAACAACAAATTCCCCGCTGGACCAGGGGGTGGGT	Db.	05-DEC-1996; 96US-0033230.	XXXX
	Db	11-JUN-1998. 04-DEC-1997; 97WO-U522629.	PX B
	Qy Qy		×

Oy 415 GGCGGTGGCTTAGCTTAGCTGGCTGGCTGGCTGGCGTGAGCGTGGGCGTAGGGTGGTGAAA 474 Db 81 GlyGlyGlyGanGlyAsmGlyGanGlyGanGlyGlyGanGlyGanGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	Oy 355 ACCGEONTA/SATRANSATRANSATRANSCOCKT/GET/GET/GET/GET/GET/GET/GET/GET/GET/GE	Oy 295 GENCTGGGGCGGGGGGGGANCANATGAN-GCOTCANTCAGCTGGCTGGCTGGCTGGCTGGTGGGGGGGGGGG	Oy 235 GGCGGAMAFAGGGGTTGCTGGGTACCACTGCCGAMTCCTGGGTTGGGTGGCTGGCTATTCT 294 Db 21 GlyGlyNsnNsnOlyLeuLewGlyThrSerArgGlnAsnAlaGlyLeuGlyGlyNsnSer 40		SEQ12-SEQ4 (1-1390) x AAW87639 (1-403)	Alignment Scores: 1,61e-161 Langth: 403 Pred. No.: 100 000 Controller: 403 Recent Enthirity: 100 000 Controller: 403 Recent Enthirity: 100 000 Mismatcher: 403 Recent Cont. Similarity: 100 000 Mismatcher: 403 Rest. 100 010 Mismatcher: 400 Deery Match: 100 000 Mismatcher: 400 Deery Match: 100 000 Gaps: 9	SQ Sequence 403 AA;	he present seq rotein (also c ypersensitive persensitive he protein, in lease resista athogens), to o provide earl orers, Lepidop ransgenic plan	PS Claim 4; Page 10-11; 94pp; English.	PT New fragments of an Erwinia hypersensitive response elicitor protein PT and related DNA - used to impart disease resistance to plants, to PT increase their growth and to control insects XX	WPI: 1999-070 N-PSDB; AAV83	PI Beer SV, Laby RJ, Wei.2;	PA (CORR) CORNELL RES FOUND INC. PA (EDEN-) EDEN BIOSCIENCE CORP. YX	PR 30-MAY-1997; 97US-0048109.	PF 28-MAY-1998; 98WO-US10874.	PD 03-DEC-1998.	AA AX WY W09854214-A2.		KW Hypersensitive response elicitor protein; hairpin protein; KW disease resistance; seed quality; insect control; corn borer; KW Lepidoptera larvae; transgenic plant;	DE A hypersensitive response elicitor protein.
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Ervi	so.	OLT 5 71093 AAY7	401	381	1255 361	1195 341	1135	301	1015 281	955 261	895	835 221	775 201	715 181	161	141	121	475 101
nia amylovora hypersensitive response elicitor #1.	~	1093 standard; Protein; 403 AA. 1093:		COGGOTATICATCCCATGATGGCCGGTGATGCCATTACATATGGCATTTGGCAAGCTG 1374	CCMTGGGGGTGATACGGCAACGGCAACCTGCAGGACGGGGGGGG	GAGGGAARGACACCAGCAGTAGGAGAGAGTCAACAAGCCAAGGCCATGATCAAAAG 1254	GSTCASCAGGTGAAAACCANTGACANTGACAATGGCAGAGCAGCGAGTGAC 1194	GSTCATTCATGACCAGNATCTGAGATGTTTGGCAGCGGAGACAGACAGACAGGCCG 1134	AGCAPAGTTCAACCCTTCTTTCGTCAATAAGCCATCGGGCARTGCGGAAGAART 1074 	GTGGGTACCGGTATCGGTATGAAAGCGGCATTCAGGGCTGAATGATATCGTACCGCA. 1014	GGGGGCAAAGGGCTGCAAACCTGAGGGGCGGGGGGGGGATACCACGAGTAGGTAAGGC 954 	Gassak/Tesakatrest/Assassatrak/Tesakatrest/Gassastrak/Gasrostroctre 84	GGAGTDA-TGARGCCCTGTGCGGCCTGATGGGTATGGTTGAGCCAACTCCTTGCCAAC 814	CAGGGCAGTTCCTCTGGGGGCAGCAGCAGCAGCAGGCGGAGGCGAGAGGCCTATAAAAAA 774	CTCCTGAAGATCTTCACCAGATAATGCAAAGCCTCTTTGGTGATGATGGCAAGATGCCACC 714	ANGSACSATTCCACCTCGGCAGAGATTCCACCTCAGATTCCAGGGACCGATGGAGAG 654	ACCAPTEANCAMCAMATROCCOCCTOMACAMCAGGGGTGGTTTAMCTCMAGGTCCCAA 594	GCGCTGAACGATATGTTAGGCGGTTCGCTGAACACGCTGGGGCTGGAAGGCGGGCAACAAT 534

Qy Db ν B Qy Db Q Db Qy 29 문 5 B 8

Q	DЬ	9	Db	Q.	B 8	DЪ	Ş	Db Qy	B 03	₽ &	SEQI	Quer DB:	Pred. Score: Percen	Alie	×	88888	X P	× 4 4	X R R	XPI	×××	X 73 X	PX	PX	PX	88	XXX
595 AACGACGATTCCACCTCCGGCACAGATTCCACCTCAGACTCCAGCGACCCGATGCAGCAG 654	121 ThrThrSerThrAnnSerProLeuAspGlnAlaLeuGly11eAsnSerThrSerGln 140	535 ACCACITCAACAACAAATTCCCCGCTGGACCAGGCGCTGGGTATTAACTCAACGTCCAA 594		475 GCGCTGAACGATATGTTAGGCGGTTCGCTGAACACGCTGGGCTCGAAAGGCGGCAACAAT 534	415 GCGGTGGCTTAGGTANGGCTTGGGTGGCTCAGGTGGCCTGGGGCAAAGAGCTTGCGAAAA 474 415 HIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	61 ThrGlyMetMetMetMetSerMetMetGlyGlyGlyGlyLeuMetGlyGlyGlyLeu 80		295 GCACTRGGGGCTGGGCGGCATCAAATCAAATCATACCGTCAATCAGCTGGCTG	25 GCOGGAATAACGGCTTGCTGCGTGCACACTGCCAGATGCTGGCGTGGCGACTGCCAATTCT 294 21 GlyGlyAsnAsnGlyLauLeuGlyThrSerArgGlnAsnAlaGlyLauGlyGlyAsnSer 40	175 ARGAGETCHARRACANTROCOTROGRACOTROCANTUTANTTETATECOCOCOCCC 234 1	SEQ12-SEQ4 (1-1390) x AAY71093 (1-403)	82.11% Indels: 21 Gaps:	Pred. April 1.61e-161 Length: 403 Score: 2079.00 Matches: 403 Seroent Similarity: 200.00N Mismatches: 0 Best Local Similarity: 100.00N Mismatches: 0	SQ Sequence 403 AA; Alignment Scores:		The parent discloses a method to impart stress resistance to plants by applying a hypersentitive reposite election in a mon-indections form to response election in a mon-indections form to response election probabilities response elections and the response election probabilities may be applicable in the second election probabilities which applicable in the second election part is the second to impart stress resistance to plants.	Disclosure: Page 7-8; 84pp; English.	Application of a hypersensitive response elicitor protein to plants to impart stress resistance	WE1; 2009-3/2000/3/. N-PSDB; AADDO668.		(EDEN-) EDEN BIOSCIENCE CORP.	05-NOV-1998; 98US-0107243.	04-NOV-1999; 99WO-US26039.	18-MAY-2000.	W0200028055-A2.	Erwinia amylovora.	Hypersensitive response elicitor: environmental stress resistance;
FT	ZX:	8 X	X X X	XX XX	XXX	a z e	AA RE	B 5	2 8 5	S & S	. P	Qy	Qy Db	Db	Qy	B 6	타 :	Q B	Qy	Db -5	0 40	7 9	da	. Q	ш	. 9	B
Peptide 169403		Rrwinia anvloyora	Hypersensitive response; insect contro hypersensitive response elicitor; plan ornamental plant.	A hypersensitive response elicitor pro-	cst entry)	AAY84854;	100		LeuGlyIle	123 CCCHROCOGO JOHINC COCCHROCHECT			1135 GGTCÅGGAGGTGAÄAÄCCGÄTGÄCAÄÄTCÄTGG 	301 GlyGlnPheMetAspGlnTyrProGluValPhe	1075 GGTCAGTTCATGGACCAGTATCCTGAGGTGTTT	1015 AGGCACAGTTCAACCCGGTTCTTTCGTCAATAAA 		241 GlyGlyLysGlyLeuGlnAsnLeuSerGlyPro	895 GGCGGCAAAGGGCTGCAAAACCTGAGCGGGCCGG			775 GGAGTCACTGATGGCGCTGATGGCCCTGATGGCCCTGATGGCCTGATGGCCTGATGGCCTGATGGCTGTCGCCCTGATGGCTGTGCTGATGGCTGTGTGTG		715 CAGGGCAGTTCCTCTGGGGGCAAGCAGCCGACCG	101 LeubeubysmerkneserGlulleMerGinser	655 CTGCTGAAGATGTTCAGCGAGATAATGCAAAAGC	

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ol; disease resistance:
int growth; vegetable; crop;
                   otein.
                                                                                                       CATTAACAATATGGCACTTGGCAAGCTG 1374
                                                                                                                                GCAGGCACGCGGTGCCGGTGGTTCTTCG 1314
                                                                                                                                                       TCAGGCGCTGAATGATATCGGTACGCAC 1014
                                                                                                                                                                                                                                                                                  GGTGGACTACCAGCAGTTAGGTAACGCC 954
                                                                                                                                                                                                                                                                                                          TGGCACGGGTCTTGACGGTTCGTCGCTG 894
                                                                                                                                                                                                                                                                                                                                  TAATGGTCTGAGCCAGCTCCTTGGCAAC 834
                                                                                                                                                                                                                                                                                                                                                           CCTGTTTGGTGATGGGCAAGATGGCACC 714
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ATGAGTCTGAATACAAGTGGGCTGGGAGCGTCAACGATGCAAATTTCTATCGGCGGTGGG 234 MELSGLLGUAATHTLIGHTHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	CAACGATGCAA	GAGCGT	CAAGTGGGCTG	TGAAT	TGAGTC	175 A	B 8	
		(03)	AAY84854 (1-403)		(1-1390) x	2-SEQ4	SEQ1	
403 00 00 00	Length: Matches: Conservative: Mismatches: Indels: Gaps:	ST HC CH L	1.61e-161 2079.00 100.00% 100.00% 82.11%	rity:	Scores: milarit Simila sh:	nent No.: ocal	Alignme Pred. N Score: Percent Best Lo Query M DB:	
				403 AA		Sequence	So	
Car	n, poinsettia, chrysanthemum,	tia, ch		pelargonium,		petunia,	38	
na, Saintp	opsis thaliana, Saint	Arabid		sorghum or		tomato,	8	
bean, melon,	ucumber app	nini, c	mpkin, zucci	squash, pum		citrus,	88	
nt, pepper, celery,	rlic, eggple	ion, ga	, radish, spinach, onion, garlic, eggplant,	dish,	li, ra	broccoli,	cc	
cabbage, brussel sprout, beet, parsnip, turnip, cauliflower,	t, parsnip,	otato, st, bee	orussel spro	, pota		endive,	88	
, cotton, sunflower,	barley, rye	wheat,	falfa, rice,	as ali		plants	8	
	egetables, o	clude v	this way in	ed in		may be	8	
e polypeptide	insects. Th	control	th, and/or	t grou	e plan	fragne	38	
esistance to plants,	rt disease	ns impa	the protein	stead,	se. In	respon	8	
cit a hypersensitive	h do not eli	s, which	de fragment	ypepti	or pol	elicit	8	
The present sequence represents a hypersensitive response elicitor polynomials. The specification describes hypersensitive response	ypersensitiv	ts ah	necification	Sequer	esent	The pr	88	
		English.	rage orio; roupp; and	0.1	4; Pag	CTGIN	×3	
				, ,		2 .	ž	
resistance to plants,	. 6	mental	vegetables and ornamental flowers	edetak	ed gro	especially veget	37	
dur		tor pol	response elicitor polypeptides :	ve res	ensiti	Hypers	3	
				4938.	SDB; AAA14938.	N-PSDB	X DR	
			ě.	3745/	000-30	WPI; 2	PR S	
		•	Niggemeyer JL;	E.	Fan	Wei 2,	2	
			HENCE CORP.	BIOSCIENCE) EDEN	(EDEN-	X P	
			0.00000.	Š			×:	
			0505010-01	20180	-1009.	05-00	g ×	
			9WO-US23181.	994	-1999;	05-OCT-1999;	PF	
					-2000.	13-APR-2000	8	
				A2 .	20452-	WO200020452-A2	χŽ	
	r claim 7"XX	ed under	/note- *claimed	>			X F	
		a under	137156	==	Ф	Peptide	FT	
				137	0	Peptide	F	
	Claim		15	121 /nc	Ф	Peptide	33	
	r claim 7"	ed under	/note= *claimed	/nc	•	Peptide	F 7	
	r claim 5"	ed under	ote- "claimed	on o			17	
	r claim 5*	unde		700	D	Pentide	33	
	r claim 5"	ed under	/note- "claimed 267403	/no 267	0	Peptide	PT	
	claim	nd under	/note= "claimed 210403	/no 210	0	Peptide	FT	
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                                                                                                                   SEQ12-SEQ4 (1-1390) x AAE06710 (1-403)
                                                                                                                                                                                                    Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       combleties encoding a hypersensitive response ellitics protein or compression and an expense of the first DNA molecule to indirect transcription of the first DNA molecule in 
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 403 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a chimeric gene that includes a first DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 13-14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rew chimerto gene, useful for controlling plant-pathogenic fungi and producing comprete first DNA according comprete first DNA encoding hypersensitive response elicitor, promoter and regulatory region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD12806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI: 2001-488791/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beer SV, Bauer DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JAN-2000; 2000US-0178565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-2001; 2001WO-US02579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypersensitive response elicitor; comycete; transgenic plant; infection
gene therapy; crop loss; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erwinia amylovora hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-007-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE06710 standard; Protein; 403 AA
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                                                               175 ATGAGTCTGAATACAAGTGGGCTGGGAGCGTCAACGATGCAAATTTCTATCGGCGGTGCG 234
MetSerLeuAsnThrSerGlyLeuGlyAlaSerThrMetGlnIleSerIleGlyGlyAla 20
                                                                                                                                                                  1.61e-161
2079.00
100.00%
100.00%
82.11%
22
                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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235 GGCGGAAATAACGGGTTGCTGGGTACCAGTCGCCAGAATGCTGGGTTGGGTGGCAATTCT 294

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1315 CTGGGTATTGATGCCATGATGGCCGGTGATGCCATTAACAATATGGCACTTGGCAAGCTG 1374

1374	EUR DOODEN EN NON MEEN DOODEN DES DOODEN DE NOOGEN DE NEGOUEN DE N	1316	2
380	CCATIOCCOGIATACCOCCANCOCCANCCIVEADCACCOSTOCOGISSITE FEET	y 1200 b 361	# 5
6	AspClyMetThrProAlaSerMetGluGlnPheAsnLysAlaLysGlyMetileLys/	34	뭐
1254	GACGGARTGACAGCAGCAGTATGGAGCAGTTCAACAAAGCCAAGGGCATGATCAAAAGG	y 1195	2
	GlyGlnGluValLysThrAspAspLysSerTrpAlaLysAlameuSerLysPrc	ω . 12	B 5
- 1		= ,	
1134 320	GTCAGTTCATGACCAGTATCCTGAGGTGTTTGGCAAGCCGCAGTACCAGAAAGGCCCG	y 1075 b 301	R 2
300	. ArgHisSerSerThrArgSerPheValAsnLysGlyAspArgAlaMetAlaLysGluIle	b 283	Db
1074	AGGCACAGTTCAACCCGTTCTTTCGTCAATAAAGGCGATCGGCGATGGCGAAGGAAAT	y 1015	QV
00		26	문 :
0 '	TGGGTACCGGTATCGGTATGAAAGCCGGGCATTCAGGGGGCTGAATGATATCGGTACGCA	0 !	2 8
954	GCCGGCAAAGGGCTGCAAAACCTGAGCGGGCCGGTGGACTACCAGCAGTTAGGTAACGCC	2 895	2 9
240	. GlyGlyLeuGlyGlyGlyGlyGlyGlyAsnAlaGlyThrGlyLeuAspGlySerSerLeu		D
894	GGACTGGGAGGTGGTCAGGGCGGTAATGCTGGCACGGTCTTGACGGTTCGTCGCTG	y 835	Ş
	lyAsn	20	B 1
	GAGTCACTGATGCGCTGTCGGGCCTGATGGGTAATGGTCTGAGCCAGCTCCTTGGCAAC		Q.
	LysLys	18	R 5
٠.	AGGGCAGTTCCTCTGGGGGCAAGCAGCCGACCGAAGGCGAGCAGAACGCCTATAAAAAA		Q.
714	CTGCTGAAGATGTTCAGCGAGATAATGCAAAGCCTGTTTGGTGATGGGCAAGATGGCACC	y 655	R 2
160	AspAspSerThrSerGlyThrAspSerThrSerAspSerSerAspProMetGlnGln	b 141	맖
654	GGACGATTCCACCTCCGGCACAGATTCCACCTCAGACTCCAGCGAGCG	y 595	60
140	ThrThrSerThrThrAsnSerProbeuAspGlnAlaLeuGlyIleAsnSerThrSerGln		Db
594	CACTTCAACAACAAATTCCCCGGCTGGACCAGGCGCTGGGTATTAACTCAACGTCCCAA	y 535	Q
120	AlaLeuAsnAspMetLeuGlyGlySerLeuAsnThrLeuGlySerLysGlyGlyAsnAsn	0 10	Di
534	CGCTGAACGATATGTTAGGCGGTTCGCTGAACACGCTGGGCTCGAAAGGCGGCAACAAT	y 475	9
100	GlyGlyLeuGlyAsnGlyLeuGlyGlySerGlyGlyLeuGlyGluGlyLeuSerAsn		밁
474	GCGCTCGCTTAGGTAATGGCTTGGGTGGCTCAGGTGGCCTGGGCGAAGGACTGTCGAAC	y 415	9
9.0	ThrGlyMatMetMetMetSerMetMetGlyGlyGlyGlyLeuMetGlyGlyGlyLeu	0 61	망
414	CCGCCATGATGATGATGACCATGATGGCGGTGGTGGGCTGATGGCGGGTGGCTTA	355	9
60	Leu =	÷	D.
354	CACTGGGGCTGGGGGGGGGTAATCAAAATGATACCGTCAATCAGCTGGGTGGCTTACTC	295	Q
40		21	DB.

9	Que DB:	Pred. Score: Percen	S X	3888	88888	8888	8888	X P X I	2222	PRXI	X Z X 3	SXRXB	X P X S	XXXX	DEX DEX	AC X X D ABB	RESI	04 B
175 ATGACTCTGANTACAAGTGGGCTGGGACCGTCAACGATGCAAATTTCTATCGGCGGTGCG 234	82.11% Indels: 23. Gaps: 3809225 (1-403)	. No.: 1.61e-161 e: 2079.00 est Similarity: 100.00% Local Similarity: 100.00%	Sequence 403 AA;	disease and desicocation, therefore reducing costs to the consumer and improving quality. The present sequence represents a hypersensitive response elicitor protein given in the exemplification of the present repents.	Penicillium, Betrytis, Phytophthora, or Erwinia) or desicontion and reministing the longestry in a fruits or vegetables. The method enables growers, warehouse packers, shippers and suppliers to process, hadde and store fruit and vegetables with reduced loses caused by sort harvest	amylovora. E stewarti, E chrysanthemi, E accouvora, Xanthomonas, pendomonas syringas, P solanacearum Bytyophthora, and Claribacter). (I) has bactericidal activity, and can be used if gene therapy. The method con be used if gene therapy in the method con be used for year the state of the method con be used for year the state of the state of the method con be used for year the state of the stat	The present invention describes methods for inhibiting post barvest disease or describing methods for inhibiting one from the prost of	Example; Page 9-10; 72pp; English.	Inhibiting post harvest disease (caused by Penicillium, Botrytis, Phytophthora, or Ervinia) or desicablion and enhancing the Longevity in a fruits or vegetables, using hypersensitive response elicitor proteins	MET 2, QLI U, KOMINCK U; MPI_ 2002-041357/05. N-9508; AMSI/10.	EN-) EDEN BIO	17-NP-2001; 201W0-US12468.	Ervinia amylovora. w0200180639-A2.	; fruit; vegetable; plant;	08-JUL-2002 (first entry) Ervinia amylovoza hypersensitive response elicitor SEO ID NO:3.	ABB09225 Standard; Protein; 403 AA. AC ABB09225;		381 LauGlyTloAsphlaketMstAlaGlyAsphlafloksnAsmMstAlalauGlyJysleu 400 1375 GGGGGGGT 1383
9	Qy Db	D 04	Oy Db	Db Oy	D 09	Qy Db	D 09	B 8	B 8	p 99	pb 49	P &	B 94	Db Oy	B Q	Db Cy	Db Oy	Db
1255 CCCAPTGGGGGTGATACCGGCAACGGCAACCTGCAGGCAGCGGGTGCGGTGCTFCTFCG 1314	1195 GACGGANTGAGACGAGCAGTATAGGAGCAGTCAACAAGCCAAGGCCATGATCAAAGG 1254 11111111111111111111111111111111111	1113 CUTPOGOCOTRONACONTRONOMATANTOGOCIANACONTRONOMACONTR	1075 GGTAGTTCATGACCAGTATCCTGAGGTGTTTGGCAAGCCGCAGTACCAGAAACCCG 1134 1111111111111111111111111111111111	1015 AGGACAGTTCAACCCGTTCTTTGGTCAATAAAGCGATCGGGCGATGGGGGATGGGGGAAGGAA	95 GTGGTACOGGTATGGGATGAAACGGGCATCAAGGCCTCAATGATATCGTACGGA 10.4 95 GTGGGTACOGGATGAAACGGGCATCAAGGCCTCAATGATATCGTACGGA 10.4 95 GTGGTATATCGTATGATATCAAGGATTATCAAGATATATCAAGATAAAAAAAA	895 GOCGGCAAAGGCTGCAAAACTGCAGCGGGGCGGTGGACTACCACACTTAGGCAACGCC 994	85 GRGGANTGGRAGTGGTDAGGGGTANTCTRGCAACGGTGTTTRAGGTTTGTGCTGT 84 81 GRGGANTGGRAGTGGTDAGGGGTANTCTRGCAACGGTGTTTGTGCTGT 84 21 GlyGlyLenGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	779 GOMETICAL INTO GASTO DE COGACO DANTOS DE METOS DE COMPACTO DE COGARCO 639 [CASGGCATTCCTCTGGGGCAAGCAGCCACCGAACGAAGCAGCAAGCA	050 CTS-TEAMARTETTCAGGAATAATCCAAACCTCTTTGGTCATATGGCAAACAGCAACCTAT 	ANDARAS SETTINGEN AND AND AND AND AND AND AND AND AND AN	ACCACTECAACAACAAGTACTCCCCCCTGGGACCAGGGGTGGGTTAACTCAACGTCCCAACTACTACTACTACTACTACTACTACTACTACTAC	GCGCTGANCGATATCTTAGCCGGTTCGCTGAACACGCTGGGCTGG	415 GOCGETGGCTRANTGCCTTGGCTGGCTCAAGGACTGGCCAAGGACTGTGCAAC 474 415 GCGCTGGCTAAGGACTGCCTGACCAAGGACTGTGCAAC 474 416 GCGCTGGCTAAGGACTGCCTAAGGACTGTGCAACAACGACTGTGCAACAACGACTGTGCAACAACGACTGTGCAACAACGACTGTGCAACAACGACTGTGCAACAACGACTGTGCAACAACGACTGTGCAACAACGACTGTGCAACAACGACTGTGCAACAACGACTGTGCAACAACAACGACTGTGCAACAACAACGACTGTGCAACAACAACAACAACAACAACAACAACAACAACAACAA	30 ACCACA TRATATRATRATRATRATA CATACATRO TRACTICA TRATAGOLITA 44 [GCACTGGGCTGGGGGGGTAATCAAAXTGATACCGTCAATCACTGGCTGGCTTGCTCT 	235 GGCGANATANGGGGTTGCTGGGTXCCAGTGCCCAANTGCTGGGTTGGGTTGGCTAGTTCT 294 236 GGCGANATANGGGGTTGCTGGGTXCCAGTGCCCAANTGCTGGGTTGGGTTGGCTAGTTCT 294 237 G1yG1yAsnAsnG1y1esuLeuG1yThrSerArgG1nAsnAlaG1y1esuG1yG1yAsnSer 40	

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В 문 8

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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                   SEQ12-SEQ4 (1-1390) x AAE18295 (1-403)
                                                                                                                                                                                                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to methods of improving the effectiveness of transpentic plants which involves either topical application of plant hypersensitive response elector (MEN) protein to the transpent plant of transpens encoding MEN. SERVING AND THE TRANSPERS CONTROLLED TO THE TRANSPERS CONTROLLED THE TRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Improving effectiveness of transgenic plants by topical application of a hypersensitive response elicitor protein to the transgenic plant or by incorporating into the plant a transgene encoding the protein .
                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 10-11; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200195724-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rypersensitive response elicitor; HRE, transgenic plant; plant growth; stress tolerance; disease tolerance; medicided flower colour; insect resistance; herbicide resistance; male sterility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE18295 standard; Protein; 403 AA
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GGGCAMAGGCTGCAMACCTGAGGGGGGGGTGGGG 	1015
GCGGCAAAGGGCTGCAAAACCTGAGCGGGCCGGTGGA 	955 261
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GGTGGTCAGGGCGGTAATGCTGGCAC 	835 221
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ITCCTCTGGGGGCAAGCAGCCGACC 	715 181
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domains having an acidic portion linked to an alpha-heix; useful for
imparting disease or stress resistance, controlling insects or
enhancing plant growth.
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N-PSDB; AAD27015.
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130..157
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s Erwinia amylovora hypersensitive response elicitor protein.	ensitive response elicitor sequences are used to enhance plant growth which encompasses greater yield. Increased in quantity of seeds produced that the right colorate and plant settler fruit colorate must plant settler truit colorate must plant settler truit colorate must plant settler truit colorate must plant settler provesses preventing direct insect damage to lant by feeding sluy, interfering with insect between settler greaters and releasing unter, preventing insects from colorating bost plants and releasing unterpretating from insect infection. The present sequence
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F-0-7-7-0-7-6-7-6-9-4

Alignment Pred. No. Score: Best Query Perce Scores:

No.:	1.6le-161	Length:	403
	2079.00	Matches:	403
nt Similarity:	100.00%	Conservative:	0
Local Similarity:	100.00%	Mismatches:	0
Match:	82.11%	Indels:	0
	23	Gaps:	0
-SEQ4 (1-1390) x AAE16447 (1-403)	AE16447 (1-403)		
175 ATGACTCTGAATACAAGTGGGCTGGGAGCGTCAACGATGCAAATTTCTATCGGCGGT	CAAGTGGGCTGGGAG	CGTCAACGATGCAAA	TTTCTATCGGCGGT

SEQ12

23 Gaps: U	
(1-1390) x AAE16447 (1-403)	
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CCARTEGOCCTGGCGGCGGTAATCAAATCATACCGTCAATCAGCTGGCTG	9 2
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GCGCTGAACGATATGTTAGGCGGTTCGCGTGAACACGCTGGGCTCGAAAGACGCGCAAACAAT 5 	20
ACCACTICAACAACAATTICCCCCTGGACCAGGCGCTGGGTATTAACTCAACGTCCAA 	40
ABCARCARTTCAACTTCAGGGAAGATTTCAACTTGAGGTTGAGGACCGACC	60
TYPOTOTGARANTTYPOACGAGNANTATICA AGCCTYTTGGTARGGCARATGGCARATGGCAC 7 	80
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895 GEOGGCAAAGGCTISCAAAACCTGAGGGCCGGTGGACTACCAGTTAGGTAACGCC

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Claim 7; Page 46-47; 69pp; English. Phila sepaner expresserize a hypersenshive response elicitor from From the abstract by the amplitude of 27 000 The elicity has a n	Imparting pathogen resistance to plants - with hypersensitive response elicitor polypeptide or protein	WPI: 1997-051614/05. N-PSDB: AAT49314.	Beer SV, Wei Z;	(CORR) CORNELL RES FOUND INC.	07-JUN-1995; 95US-0475775.	05-JUN-1996; 96WO-US08819.	19-DBC-1996.	W09639802-A1.	Erwinia amylovora.	(Hypersensitive response; elicitor; Erwinia amylovora; plant; disease-resistence; Escherichia coli; difiltration, vitus; bacterium; fungus; pathogen; biological control agent.	Hypersensitive response elicitor protein.	30-MAR-1997 (first entry)	AAW06598;	AAW06598 standard; Protein; 385 AA.	017 11		1375 GGCGCGGCT 1383	1315 CMCGCTATTCARTGCCCATCATGCCCGCTATTCACCATTACCAACTTGCCAACTTGCCAACTTG 1374 11111111111111111111111111111111111	ProMetalaclyaspintclyasnclyasnceucinalaargolyalaclyclyserser	CCCATGGGGGTGATACCGGCAACGGCAACCTGCAGGACGACGCGGTGGCGGTGGTTCTTCG	1195 GACGANTGACACCACCAGTWCGAGCAGTTCACAAACCAAGCCATCAAAACC 1254 341 ASGGlyMetThrFroAlaSerMetGlucinPheAsnLysAlaLySGlyMetHatysArg 360	1135 GDTOAGGAGGTGAAAACGARGACAAATAYGGGGCAAACACTGAGCAAGCCAAGTGAC 1194 321 GLYGLOGLWALLysthrAspAspLysSertrpAlaLysAlaLeuSerLysProAspAsp 340	1075 GSTRANTICANGAGARTATCITSAGGISTATIGGGAAGCCCGAGTACGAGAAGCCCCG 1134 301 GLYGLIDPHAWELASPGLATYFETGGLUVALPHAGLYLYSPICOGLUYSGLYPICO 320	1015 MOCANGETVANCCOTTCTTTCTTCATTAMAGGCATGGGGGGATGGCCAMGGAAGTC 1074 281 ArghisSerSerThrArgSerTheValAsnLysGlyAspArgAlametAlaLysGluile 300	955 GTOGOTACCOSTATCOSTATCOSTACCOSCONTTC/AGCCCTGAATGATCCTGACCOTACCOSC 1014 261 Val01yThroly1leGlyNeetLysAlaGly1leGlnAlaLeuAsnAsplleGlyThrHis 280	241 GlyGlyLysGlyLeuGlnAsnLeuSerGlyFroValAspTyrGlnGlnLeuGlyAsnAla 260
Qy Qy	9	P 9	D	9	Db	Qy	Db	Qy	Db	Qy Db	Q	Db	Qy	Db	Qy	B .	Qγ	B 99	u	9	SEQ12-SE	Score: Percent Best Loc	SQ Seq Alignmen		CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CC Con

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Erwinia amyLovora, with a mol.wt. of 37,000. The elicitor has a of 4.3, thermostability at 100 deg C for at least 10 min, and

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conclains on cysteline. The alicitor may be used in a new method for appariture plants of requirement of the alicitor plants of the plants of the alicitor plant
plants.
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Sequence 385 AA

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535 121	475 101	415	61	295 41	235 21	175	SEQ4	ent Sc No.: t Simi ocal S
ACCACTTCAACAA	GCGCTGAACGATA	GGCGGTGGCTTAG	ACCGGCATGATGAT ThrGlyMetMetMe	GCACTGGGGCTGG	GGCGGAAATAACG GlyGlyAsnAsnG	ATGAGTCTGAATAC	(1-1390)	ores: larity: imilarity:
CAAATTCCCCGCTG	RGTTAGGCGGTTCG stLeuGlyGlySer	TAATGCCTTCGGT	FGATGATGAGCATG tMetMetSerMet	GCGCGGTAATCAA yGlyGlyAsnGlni	GTTGCTGGGTACC	MAGTGGGCTGGGA mSerGlyLeuGly	x AAW06598 (1-385)	6.33e-154 1986.00 99.74% 99.74% 78.44%
3ACCAGGCGCTGGGTA 	DTGAACACGCTGGGCT	GCTCAGGTGGCCTGG 	ATGGGCGGTGGTGGGG 	AATGATACCGTCAATC NsnAspThrValAsnG	AGTCGCCAGAATGCTC BerArgGlnAsnAlac	GCGTCAACGATGCAAA 		Length: Matches: Conservative: Mismatches: Indels: Gaps:
ACCACTTCAACAACAACAATTOCCCGCTGGACCAGGGGGTGGGTATTAACTCAACGTGGCAA 	GCCCTGAACGATATGTTAGGCGCTTCGCTGAACACGCTGGCTCGAAAGGCGGCAACAAT 	GCCGGTCGCTTAGGTAATGGCTTGCGTGGCCTCAGGTGGCCTGGGCGAGGACGACTGTGGAAC 	ACCGCCATGATGATGATGATGACATGACGCGCTGCTGGCCGCTGATGGGCGGTGGCTTA	GCACTGGGGTGGGGGGGGTAATCAAAATGATACGGTCAATCACCTGGCTGG	GGCGGAAATAACGGGTTGCTGGGTTACCACTGGCAGAATGCTGGGTTGGGTTGGGTTGGGAATTCT 	ATGAGTCTGAATACAAGTGGGCTGGGAGGGTCAACGATGCAAATTTCTATGGGGGGCTGGG 		385 0 1
594 140	534 120	100	414 80	354 60	294 40	234 20		

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Claim The h	Hypersensi amylovora inhibitors	WPI; 1	Bauer	(CORR	01-JUL-	30-JUN	20-JAN	W0940	Misc-	Key Misc-	Erwin	Harpi Rosac hyper	Erwin	11-JUL	AAR45	ESULT 12 LR45751 AAR45	380		in	1195	1135 321	1075 301	1015 281	955 261	
 lovora moine a 40-f	presensitive response elititor protein derived from Erwinia mylavora - and twa encoding it, waskil for developing harpin nhibitors to prevent e.g. fire blight of fruit	994 -	DW. Beer SV, Collmer A, He S, Laby R, Wei Z:) CORNELL RES FOUND INC.	L-1992; 920S-0907935.	N-1993; 93WO-US06243.	N-1994.	1546-A.	"corresponds to CAC codon	iocation/Qualifiers difference 372 /notes "Corresponds to CaC redoo"	ia amylovora.	resease the response of the bush the bight; bright party party party proposition; response of the bight; bright party party proposition; but the diefers free bight; bright resettion; bright resettion and pathogenicity; htpN; gene cluster; ds.	ia amylovora harpin.	L-1994 (first entry)	751;	751 standard; Protein; 385 AA.	GTGGGTATCATCCA 130 HIHIHIHIHIHI GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT		CCCATGGCGGGTGATACCGGCAACGGCAACCTGCAGGCACGCGGTGCCGGTGGTTCTTCG 1314	GOCGGATGACACCAGCAGTATGSACCAGTCAACAAGCCCAGGGCATGATCAAAAGG 1254 	GUTCHGGAGTGANANCCGATKOKANATKATGGGCNANGCATGNGCANGCANGCGAGTGAC 1194	GIYGInPheMetAspdlnTyreroclavGfyTTfGcAAGCGGAYPACDAGAAGCGCC 1134 	AGGEALAGTTCAACCCSTTGCGTCAATAAAGGGATCGGGGGATGGGGGAGGAATC 1074 	\(\text{VisignAccograncogranchahaccagacArroAccagacarraArcararroArroAccagac}\) 1014 \[\] \(\text{IIII} \) \(\text{IIIII} \) \(\text{IIII} \) \(\text{IIII} \) \(\text{IIII} \) \(\text{IIIII} \) \(\text{IIII} \) \(\text{IIIII} \) \(\text{IIIII} \) \(\text{IIII} \) \(\text{IIIII} \) \(\text{IIIII} \) \(\text{IIII} \) \(\text{IIIII} \) \(\text{IIIIII} \) \(\text{IIIIII} \) \(\text{IIIIII} \) \(\text{IIIIIII} \) \(\text{IIIIIIIIIII} \) \(IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	

8×888888 degenerate oligonuclastide probe corresponding to amino acids 9-15 at the H-terminus of harpin. The 4kb protein encoded by the hap gene is a hypersonsitive response elicitor protein. The harpin is thought to be an archetype for HR elicitors from phytopathogenic bacteria.

Sequence 385 AA;

2007 2007 21 2007	15	uery Match: 77.49	est Local Similarity: 98.70	ercent Similarity: 98.96	core: 1962.	red. No.: 5.78e	Alignment Scores:
		*	œ	de	00	-152	
	Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:	
	0	_	ω	۳	381	385	

our wo	2.78e-124	rength:	CRF
ore:	1962.00	Matches:	381
rcent Similarity:	98.96%	Conservative:	-
st Local Similarity:		Mismatches:	w
ery Match:		Indels:	_
	15	Gaps:	0
Ql2-SEQ4 (1-1390) x AAR45751 (1-385)	AAR45751 (1-385)		
175 ATGAGTCTGAATACAAGTGGGGTGGGAGGGTCAAGGATGCAAATTTCTATCGGCGGTG	ACAAGTGGGCTGGGAG	CCTCAACGATGCAAA	TITCTATCGGCGGTG
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175 ARROGETICAMAN ANAFORDE CORROGETICAMATE PROPERTOR 24. 175 ARROGETICAMA PROPERTOR CORROGETICAMATE PROPERTOR CORROGETICAMA PROPERTOR CORROGETICAMA PROPERTOR CORROGETICAMAN PROPERTOR CORROGETICAMAN AND CORROGETICAMAN AND CORROGETICAMAN AND CORROGETICAMAN AND CORROGETICAMAN CO	SEQ4	("SEQ4 (1"1390) X AAK45/51 (1-385)	
1 Medicina de la mentra de la manda de la medicina del medicina de la medicina del med	175	ATGAGTCTGAATACAAGTGGGCTGGGAGCGTCAACGATGCAAATTTCTATCGGCGGTGCG	34
235 GECCOANTANOSCOTIVETOCOSTACCACCICCOALATICTEGGTTVGGTTVGGTTVGGTTVGGTTVGGTTVGGTTVGG	ш	MetSerLeuAsnThrSerGlyLeuGlyAlaSorThrMetGlnIleSerIleGlyGlyAla	9
21 GlyGlyManAshGlyJeucuGlyThrServjolnashAlGlyHurlJflHHHHH 4 29 GLYGGGGGGGGGGGAATCAAAAYGATACGGTCAAYCACGTGGCTGACTC 354	235	GGCGGAAATAACGGGTTGCTGGGTACCAGTCGCCAGAATGCTGGGTTGGGTGGCAATTCT	94
295 GCACTGGGGCTGGGCGGGTAATCAAAATGATACCGTCAATCAGCTGGCTTGCTT	21	GlyGlyAsnAsnGlyLeuLeuGlyThrSerArgGlnAsnAlaGlyLeuGlyGlyAsnSer	0
	295	GCACTGGGCTGGGCGGCGAATCAAAATGATACGCTCAATCAGCTGGCTTGCTT	54

61	355	4
61 ThrGlyMetMetMetMetSerMetKetGlyGlyGlyGlyLeuMetGlyGlyGlyLeu 80	355 ACCGGCATGATGATGATGATGATGGGCGGTGGTGGGCTGATGGGCGGTGGCTTA 414	41 AlaLeuGlyLeuGlyGlySlyAsnGlnAsnAspThrValAsnGlnLeuAlaGlyLeuLeu 60
0	14	0

535	101	475
535 ACCACTTCAACAACAAATTCCCCGCTGGACCAGGCGCTGGGTATTAACTCAACGTCCCAA 594	101 AlaLeuAsnAspMetLeuGlyGlySerLeuAsnThrLeuGlySerLysGlyGlyAsnAsn 120	475 GCGCTGAACGATATGTTAGGCGGTTCGCTGAACACGCTGGGCTCGAAAGGCGGCAACAAT 534
594	120	534

14	59	12
141 AsnAspAspSerThrSerGlyThrAspSerThrSerAspSerSerAspProMctGlnGln 160	595 AACGACGATTCCACCTCCGGCACAGATTCCACCTCAGACTCCAGCGACCCGATGCAGCAG 654	121 ThrThrSerThrThrAsnSerProLeuAspGlnalaLeuGlyIleAsnSerThrSerGln 140
ő	A	0

161	655	141
161 LeuLeuLysMetPheSerGluIleMetGlnSerLeuPheGlyAspGlyGlnAspGlyThr 180	655 CTGCTGAAGATGTTCAGCGAGATAATGCAAAGCCTGTTTGGTGATGGGCAAGATGGCACC 714	
80	14	60

1	Ut
1 GlnGlySerSerGlyGlyLysGlnProThrGluGlyGluGlnAsnAlaTyrLysLys 200	5 CAGGGCAGTTCCTCTGGGGGCAAGCCGACCGAAGGCGAAGGCAGAACGCCTATAAAAAAA 774
6	4

71

201	775
201 GlyValThrAspAlaLeuSerGlyLeuNetGlyAsnGlyLeuSerGlnLeuLeuGlyAsn 220	775 GGAGTCACTGATGCGCTGTCGGGCCTGATGGGTAATGGTCTGAGCCAGCTCCTTGGCAAC 834
20	34

280	261 ValGlyThrGlyIleGlyMetLysalaGlyIleGlnalaLeuAsnAspIleGlyThrHis 280	261
1014	955 GTGGGTACCGGTATCGGTATGAAAGCGGGCATTCAGGCGCTGAATGATATCGGTACGCAC 1014	955
260	241 GlyGlyLysGlyLeuArgGlyLeuSerGlyProValAspTyrGlnGlnLeuGlyAsnAla 260	241

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Ane.	This sequence represents a hypotressitive response slicitor from Ervinia Chysanthami, with a soli, w. of 34,000. The elicitor in themsetable, has a slicine content of over 100 and has no cyste tresistance to plants. My spilotation of the elicitor in a non- infections from the plant cells, by spraying, injection, loss infections from the plant cells, by spraying, injection, loss absalso, of plant infection with recombinant better in (more at licitors as a biological control spent, to allior Accombinant potent infiltration into the plants. The method confers within potent infiltration into the plants. The method confers when the plants of thosis of the plants of crops and ornamental plants.	88888888888
	response efficient porypeptide of Claim 4: Page 44; 69pp; English.	P X P
	imparting pathogen resistance to plant response elicitor polypeptide or prote	PTXX
	WPT; 1997-0516 N-PSDB: AAT493	R R X
	(CORR) CORNELL	XX PA
	07-JUN-1995; 95US-0475775.	X PR
	05-JUN-1996; 96WO-US08819.	X PS
	19-DEC-1996.	PD.
	WO9639802-A1.	Y P X
	Erwinia chrysanthem	SS
	Hyperemaitive response, elicitor; Ervinia chrysanthemi; plant; disease-resistance; Escheritchia coli; infiliatrion; virus; bacterium; fungus; pathogen; biological control agent.	2 2 2 3 2 3 3 3
	Hypersensitive resp	XX XX
	30-MAR-1997 (first entry)	X D X
	AAW06597;	AC X
	157 13 6597 ANW06597 standard; Protein; 338 AA.	RESULT AAW065 ID A
	380 gTrpvalLeuMetPro 385	DЬ
	1315 CTGGGTATTGATGCCA 1330	Qy
1314	1255 CECATROGGGGTARTACGGCAACGGCAACCTCCAGGCACGCGGGGCGCGGGTGCCGGTGTCTCGGGGGGGG	Qу
1254	1195 GAGGANGBAGCSAGCAGRAGGAGGAGGTGAGCAAAGGCAAGGGGATGATGAAAAGG 1195 GAGGANGBAGCAGCAGGAGGGAGGAGGGAAAAGGCAAGGGGATGATGAAAAGG 111111111111111111111	Qу
1194	1135 GCTPAGGAGGTSAAACCGATGACAAATCATGGGCAAAACACTGACCAAGCAAG	Qy Db
1134	1075 GEPAGTTCATGAGCAGCAGFATCTTGAGGTGTTTGGCAAGCGGGAGFACCAGAAGCGCGG 1076 GEPAGTTCATGAGCAGCAGTGTTTTGGCAAGCGCGAGFACCAGAAGCGCGG 11111111111111111111111111	Qy Db
1074 300	1015 AGGCACAGTTCAACCCGTTCTTTTCGTCAATAAAGGCGATTCGGGCGATGGCGAAGGAATTC	Qу

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1012	195	52	892 175	on t	832	72	129	9	676	99	6	97	556	8.3	496	6.4	6	56	376	39	316	21	268	1	211	-SEQ4	d. No.: ore: ore: orent Si t Local ary Matc	Sequen
CACAGGCACAGTTCAACCCGTTCTTTCGTCAATAAAGC	AlaileGlyMetGlyValGlyGlnAsnAlaAlaieu	GCCGTGGGTACCGGTATGAAAGCGGGCATT	CTGCGCGGCAAAGGCTGCAAAACCTGAGCGGG euGlyAlaGlyGlyLeuGlnGlyLeuSerGly		AACGGGGGACTGGGAGGTGGTCAGGGCGGT	AAAGGAGTCACTGATGCGCTGTCGGGCCTGATGGGTAATGGTCTGAGCC	ACCCAGGCATTCTTTGGGGCAAGCAACCAACCAAACGAAGCAACCAAC	AlaLeuAspAspLeuLeuGlyHisAspThrValThrLys	AATGCAAAGCCTGTTTGGT	yAspAlaLeuSer	AGATTCCACCTCAGACTCCAGCGACCGATGCAGCAG		CCGCTGGACCAGGCGCTGGGTATTAACTCAACGTCCCAAAAC	GlyAlaGlnGlyAl	AACACGCT	ιά	PCAGGTGG		CATGATGGGCGGTGGTGGGCTGATGGGCGGTGGC	LysLeuSerSerThrIleAspLysLeuThrSerAlaLeu	AATCAAAATGATACCGTCAATCAGCTGGCTTACTCACCGGCATGATGA	e E	AGAATGCTGGGTTGGGTGGCAATTCTGCA	AlaHis	ATGCAAATTTCTATCGGCGGTGCGGGGGGGGAAATAACGGGTTGCTGGGTACCA	1 (1-1390) x AAW06597 (1-338)	Scores: 2.18e-50 Length: 718.50 Matches: 2.978 Conservativ 22.979 Missatches: 42.829 Missatches: 18 Gaps: 1668.5	ance 338 AA;
GATCGGCGATGGCGAAGGAA 1071	AlaLeuSerAsnValSerTh	CAGGCGCTGAATGATATCGGTACG 1011	CCGGTGGACTACCAGCAGTTAGGTAAC 951 ::: AlaGlyAlaPheAsnGlnLeuGlyAsn 194	17	ACGGTTCGTCG 89	GETCTGAGCCAGCTCCTTGGC 831	Ly 1	ln 12	GATGGGCAAGATGGC 71	EysMetPheAspLys 1	GCTGAAGAT	SerGly 98	GACGATTO	aSerAsnLeuLeuServalProLys 96	ACCACTTCAACAACAAATTCC 555		2	PheGlyGlyAlaLeuAlaGlnGly 63	GTAAS	ThrserMetMet 55	ī	SerLeuGlySerSerValAsp 38		SlyValSerGlyLeuGlyAla 20	GGTTGCTGGGTACCAGTCGC 267		338 173 :- 41 :- 111 79	

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1072 ATCGGTCAGTTCATGGACCAGTATCCTGAGGTGTTTGGCAAGCCGCAGTACCAGAAAGCC 1131

В Ş 망 9 Вb 8 Db 9 В 9

335 LeuAlaAsnAla 338

1372 CTGGGCGCGGCT 1383

315

Query Percer Best 1 Alignment Scores: Pred. No.: S

Sequence

338 AA;

Page 15

SEQ12

DB:

1312 TOSCINGGTATIGATICCATGATGCCCGGTGATGCCATTAACAATATGCCACTTGGCAAG 1371

SerLeuGlyIleAspAlaAlaValValGlyAspLysIleAlaAsnMetSerLeuGlyLys 334

9 8 Š,

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seq12-seq4.n2p.rag

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Alijamani Socesi 2.18e-50 Length: 338 Prof. Mo.: 2.18e-50 Length: 338 Socesi: State 3.7 Socesi: 12.7 Socesi: 12.7 Socesi: 12.7 Soc. 3.8 Soc. 3.8	This sequence represents a novel Ersinia chrysanthem; protein, hrph-cb, that clicits a hypersonistive response in plants. The encoding pok can be used for imparting pathogen resistance to plants. By transforming a plant with a vector containing the DNA and a pathogen-inducible promoter. Sequence 338 AA:	DAM encoding Ervinia chrysanthemi hypersemsitive response protein htpN - useful for laparting perhopen resistance to plants claim 2: Column 29-30: 27pp; English.	Baser D. collmer A: werl 1999-69852/06/ N-9881 MY7304, AWT3507.	07-70H-1995; 9989-048438. 07-70H-1995; 9989-048438. (COMR) OCHMRLL RES FOUND INC.	USS950015-A. 15-DDC-1998.	Nypasantitvo esponse aicito protein hppreb, pahogan resistance; plant: Transformation pahogan inducible proceder. Ervinia chrysantomi.	20-RH92407; 20-RH9299 (first entry) 20-RH9299 (first entry) E. Ohrysanthemi Hiph-EdH protein.	RESULT 13 ANA PARAMETAN Standard; Protein: 338 AA. XX	1372 CTGGGCGCGCT 1383 1372 CTGGGCGCGCT 1383 335 LeuAlabsnAla 338	1312 TOGOTGGGTMTTGATGCCATGATGCCGGTGATGCCATTAACAATATGGGACTTGGCAGE 1371 1111	AGGCCATGCCGCTGATACCGCAACCGCAACCTGCAGGCACGCGCTGCCGGTGCTCT :::	1192 GACGACGGAATGACACCAGCCAGTWIGGAGCAGTCGAACAAAGCCCAAGGGCCTGATCAAA 1251 	1.132 COGGGTGAGGGGGAAACCAGGGAAACCAGGGGAAACCAGGGGGGAAACCAGGGGGAAAT 1.9.1 2.25 GIYTINSSATSSATSSATSSATSSATSSATSSATSSATSSATSSA	235
Oy 1192 GAGGACGAMTGAAACGATGAAA		952	Db 168 Oy 892 CTGGGCGGCAAAGGGCTGCAAAACCTGAG	Oy 772 AANGGAGTCACTANTGCGCTGTTGGGGCTT IIIIII 1111III 111IIIIIII Db 149 SerGlyValAsnasnAlaLeuSerSerII Oy 832 AACGGGGGACTGGGAGGTGGTCAGGGCGC	Oy 712 ACCCAGGGCAGTTCCTCTGGGGGCAAGCA Db 129 LeuAlaAsnSerMetLeuAsnAlaSerGI	Db 99 GlyaspAlaLeuSer	Db 97	5 8 3 4 9 6 5 5 6 7 7 8 7 9 7 9 7 9 7 9 7 9 7 9 9 7 9 9 9 9	Db 64 LeuGlyAlaSerSerLysGlyLeuGl	376 56		Qy 268 CAGAATGCTGGGTTGGGTGGCAATTC	211	SEQ12-SEQ4 (1-1390) x AAWB2407 (1-338)

1132 CCGGGTCAGGAGGTGAAAACCGATGACAAATCATGGGCAAAAGCACTGAGCAAGCCAGAT 1191

255 GlyTrpSerSerProLysThrAspAspLysSerTrpAlaLysAlaLeuSerLysProAsp 274

832 AACGUGGGACTUGGAUGTGUTCAGGGCGGTAATGCTGGCACGGGTCTTGACGGTTCGTCG 891

-SerGlyPheSerGlnProSer 174

